

SEQUENCE LISTING

<110> Ganymed Pharmaceuticals AG
 TURECI, Ozlem
 SAHIN, Ugur
 HELFTENBEIN, Gerd
 SCHLUTER, Volker

<120> Identification of Tumour-Associated Cell Surface Antigens for Diagnosis and Therapy

<130> VOS-203

<140> US10/573,229

<141> 2006-03-24

<150> PCT/EP2004/010697

<151> 2004-09-23

<150> DE 103 44 799.7

<151> 2003-09-26

<160> 312

<170> PatentIn Version 3.1

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Ser Val Met Asn Gly Ile Cys Leu Leu Leu Ala Ala Val Thr Val Lys
20           25           30

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Leu Tyr Ser Ser Phe Asp Phe Asn Cys Pro Cys Leu Val His Tyr Asn
35           40          45

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Ala Leu Tyr Gly Leu Gly Leu Leu Leu Thr Pro Pro Leu Ala Leu Phe
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Trp Arg Arg Pro Ala Gly His Arg Arg Lys Asp Pro Gly Ile Ile Arg
85 90 95

Tyr Met Cys Ser Ser Val Leu Gln Arg Ala Leu Ala Ala Pro Leu Val
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Trp Ile Leu Leu Ala Leu Leu Asp Gly Lys Cys Phe Val Cys Ala Phe
115 120 125

Ser Ser Ser Val Asp Pro Glu Lys Phe Leu Asp Phe Ala Asn Met Thr
130 135 140

Pro Ser Gln Val Gln Leu Phe Leu Ala Lys Val Pro Cys Lys Glu Asp
145 150 155 160

Glu Leu Val Arg Asp Ser Pro Ala Arg Lys Ala Val Ser Arg Tyr Leu
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Arg Cys Leu Ser Gln Ala Ile Gly Trp Ser Val Thr Leu Leu Leu Ile
180 185 190

Ile Ala Ala Phe Leu Ala Arg Cys Leu Arg Pro Cys Phe Asp Gln Thr
195 200 205

Val Phe Leu Gln Arg Arg Tyr Trp Ser Asn Tyr Val Asp Leu Glu Gln
210 215 220

Lys Leu Phe Asp Glu Thr Cys Cys Glu His Ala Arg Asp Phe Ala His
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Arg Cys Val Leu His Phe Phe Ala Ser Met Arg Ser Glu Leu Gln Ala
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Val Pro Glu Pro Pro Glu Gly Leu Asp Ser Gly Ser Gly Lys Ala His
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Leu Arg Ala Ile Ser Ser Arg Glu Gln Val Asp Arg Leu Leu Ser Thr
290 295 300

Trp Tyr Ser Ser Lys Pro Pro Leu Asp Leu Ala Ala Ser Pro Gly Leu
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Arg Leu Ser Gln His Thr Asp Val
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<400> 22

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Gly Gly Trp Leu Leu Ser Leu Val Arg Gly Leu Leu Pro Cys Leu Pro
 35 40 45

Pro Gly Ala Arg Thr Ala Glu Gly Pro Ile Met Val Leu Ala Gly Pro
 50 55 60

Leu Ala Val Ser Leu Leu Leu Pro Ser Leu Thr Leu Leu Val Ser His
 65 70 75 80

Leu Ser Ser Ser Gln Asp Val Ser Ser Glu Pro Ser Ser Glu Gln Gln
 85 90 95

Leu Cys Ala Leu Ser Lys His Pro Thr Val Ala Phe Glu Asp Leu Gln
 100 105 110

Pro Trp Val Ser Asn Phe Thr Tyr Pro Gly Ala Arg Asp Phe Ser Gln
 115 120 125

Leu Ala Leu Asp Pro Ser Gly Asn Gln Leu Ile Val Gly Ala Arg Asn
 130 135 140

Tyr Leu Phe Arg Leu Ser Leu Ala Asn Val Ser Leu Leu Gln Ala Thr
 145 150 155 160

Glu Trp Ala Ser Ser Glu Asp Thr Arg Arg Ser Cys Gln Ser Lys Gly
 165 170 175

Lys Thr Glu Glu Glu Cys Gln Asn Tyr Val Arg Val Leu Ile Val Ala
 180 185 190

Gly Arg Lys Val Phe Met Cys Gly Thr Asn Ala Phe Ser Pro Met Cys
 195 200 205

Thr Ser Arg Gln Val Gly Asn Leu Ser Arg Thr Ile Glu Lys Ile Asn
 210 215 220

Gly Val Ala Arg Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val
 225 230 235 240

Ile Ser Ser Gln Gly Glu Leu Tyr Ala Ala Thr Val Ile Asp Phe Ser
 245 250 255

Gly Arg Asp Pro Ala Ile Tyr Arg Ser Leu Gly Ser Gly Pro Pro Leu
 260 265 270

Arg Thr Ala Gln Tyr Asn Ser Lys Trp Leu Asn Glu Pro Asn Phe Val
 275 280 285

Ala Ala Tyr Asp Ile Gly Leu Phe Ala Tyr Phe Phe Leu Arg Glu Asn
 290 295 300

Ala Val Glu His Asp Cys Gly Arg Thr Val Tyr Ser Arg Val Ala Arg
 305 310 315 320

Val Cys Lys Asn Asp Val Gly Gly Arg Phe Leu Leu Glu Asp Thr Trp
 325 330 335

Thr Thr Phe Met Lys Ala Arg Leu Asn Cys Ser Arg Pro Gly Glu Val
 340 345 350

Pro Phe Tyr Tyr Asn Glu Leu Gln Ser Ala Phe His Leu Pro Glu Gln
 355 360 365

Asp Leu Ile Tyr Gly Val Phe Thr Thr Asn Val Asn Ser Ile Ala Ala
 370 375 380

Ser Ala Val Cys Ala Phe Asn Leu Ser Ala Ile Ser Gln Ala Phe Asn
385 390 395 400

Gly Pro Phe Arg Tyr Gln Glu Asn Pro Arg Ala Ala Trp Leu Pro Ile
405 410 415

Ala Asn Pro Ile Pro Asn Phe Gln Cys Gly Thr Leu Pro Glu Thr Gly
420 425 430

Pro Asn Glu Asn Leu Thr Glu Arg Ser Leu Gln Asp Ala Gln Arg Leu
435 440 445

Phe Leu Met Ser Glu Ala Val Gln Pro Val Thr Pro Glu Pro Cys Val
450 455 460

Thr Gln Asp Ser Val Arg Phe Ser His Leu Val Val Asp Leu Val Gln
465 470 475 480

Ala Lys Asp Thr Leu Tyr His Val Leu Tyr Ile Gly Thr Glu Ser Gly
485 490 495

Thr Ile Leu Lys Ala Leu Ser Thr Ala Ser Arg Ser Leu His Gly Cys
500 505 510

Tyr Leu Glu Glu Leu His Val Leu Pro Pro Gly Arg Arg Glu Pro Leu
515 520 525

Arg Ser Leu Arg Ile Leu His Ser Ala Arg Ala Leu Phe Val Gly Leu
530 535 540

Arg Asp Gly Val Leu Arg Val Pro Leu Glu Arg Cys Ala Ala Tyr Arg
545 550 555 560

Ser Gln Gly Ala Cys Leu Gly Ala Arg Asp Pro Tyr Cys Gly Trp Asp
565 570 575

Gly Lys Gln Gln Arg Cys Ser Thr Leu Glu Asp Ser Ser Asn Met Ser
580 585 590

Leu Trp Thr Gln Asn Ile Thr Ala Cys Pro Val Arg Asn Val Thr Arg
595 600 605

Asp Gly Gly Phe Gly Pro Trp Ser Pro Trp Gln Pro Cys Glu His Leu
610 615 620

Asp Gly Asp Asn Ser Gly Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp
 625 630 635 640

Ser Pro Arg Pro Arg Cys Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile
 645 650 655

His Ile Ala Asn Cys Ser Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser
 660 665 670

Trp Ala Leu Cys Ser Thr Ser Cys Gly Ile Gly Phe Gln Val Arg Gln
 675 680 685

Arg Ser Cys Ser Asn Pro Ala Pro Arg His Gly Gly Arg Ile Cys Val
 690 695 700

Gly Lys Ser Arg Glu Glu Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro
 705 710 715 720

Val Pro Ile Phe Trp Ala Ser Trp Gly Ser Trp Ser Lys Cys Ser Ser
 725 730 735

Asn Cys Gly Gly Gly Met Gln Ser Arg Arg Arg Ala Cys Glu Asn Gly
 740 745 750

Asn Ser Cys Leu Gly Cys Gly Val Glu Phe Lys Thr Cys Asn Pro Glu
 755 760 765

Gly Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr Pro Trp Leu Pro
 770 775 780

Val Asn Val Thr Gln Gly Gly Ala Arg Gln Glu Gln Arg Phe Arg Phe
 785 790 795 800

Thr Cys Arg Ala Pro Leu Ala Asp Pro His Gly Leu Gln Phe Gly Arg
 805 810 815

Arg Arg Thr Glu Thr Arg Thr Cys Pro Ala Asp Gly Ser Gly Ser Cys
 820 825 830

Asp Thr Asp Ala Leu Val Glu Val Leu Leu Arg Ser Gly Ser Thr Ser
 835 840 845

Pro His Thr Val Ser Gly Gly Trp Ala Ala Trp Gly Pro Trp Ser Ser
 850 855 860

Cys Ser Arg Asp Cys Glu Leu Gly Phe Arg Val Arg Lys Arg Thr Cys
 865 870 875 880

Thr Asn Pro Glu Pro Arg Asn Gly Gly Leu Pro Cys Val Gly Asp Ala
 885 890 895

Ala Glu Tyr Gln Asp Cys Asn Pro Gln Ala Cys Pro Val Arg Gly Ala
 900 905 910

Trp Ser Cys Trp Thr Ser Trp Ser Pro Cys Ser Ala Ser Cys Gly Gly
 915 920 925

Gly His Tyr Gln Arg Thr Arg Ser Cys Thr Ser Pro Ala Pro Ser Pro
 930 935 940

Gly Glu Asp Ile Cys Leu Gly Leu His Thr Glu Glu Ala Leu Cys Ala
 945 950 955 960

Thr Gln Ala Cys Pro Glu Gly Trp Ser Pro Trp Ser Glu Trp Ser Lys
 965 970 975

Cys Thr Asp Asp Gly Ala Gln Ser Arg Ser Arg His Cys Glu Glu Leu
 980 985 990

Leu Pro Gly Ser Ser Ala Cys Ala Gly Asn Ser Ser Gln Ser Arg Pro
 995 1000 1005

Cys Pro Tyr Ser Glu Ile Pro Val Ile Leu Pro Ala Ser Ser Met
 1010 1015 1020

Glu Glu Ala Thr Asp Cys Ala Gly Phe Asn Leu Ile His Leu Val
 1025 1030 1035

Ala Thr Gly Ile Ser Cys Phe Leu Gly Ser Gly Leu Leu Thr Leu
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Ala Val Tyr Leu Ser Cys Gln His Cys Gln Arg Gln Ser Gln Glu
 1055 1060 1065

Ser Thr Leu Val His Pro Ala Thr Pro Asn His Leu His Tyr Lys
 1070 1075 1080

Gly Gly Gly Thr Pro Lys Asn Glu Lys Tyr Thr Pro Met Glu Phe
 1085 1090 1095

Lys Thr Leu Asn Lys Asn Asn Leu Ile Pro Asp Asp Arg Ala Asn
 1100 1105 1110

Phe Tyr Pro Leu Gln Gln Thr Asn Val Tyr Thr Thr Thr Tyr Tyr
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Pro Ser Pro Leu Asn Lys His Ser Phe Arg Pro Glu Ala Ser Pro
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Gly Gln Arg Cys Phe Pro Asn Ser
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<400> 24
 gttgcacgtc ttgaactcca c 21

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Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
20          25          30

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Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
35          40          45

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Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
50          55          60

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Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
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Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
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Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
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Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
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Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
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Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
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Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
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Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
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Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
195 200 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
210 215 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
225 230 235 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
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Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
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<212> DNA
<213> Artificial Sequence

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<223> Oligonucleotide

<400> 27
ggagtagtca ctcagtagca gc

<210> 28
 <211> 19
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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 28
 gaactcatca aagcagacg 19

<210> 29
 <211> 1528
 <212> DNA
 <213> Homo sapiens

<400> 29
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 tctgtgcgtc ctgcaccac atctttctct gtccctcct tgccctgtct ggaggctgct 180
 agactcctat cttctgaatt ctatagtgcc tgggtctcag cgcagtgccg atggtggccc 240
 gtccttgtgg ttctctctta cctggggaaa taaggtgcag cggccatggc tacagcaaga 300
 cccccctgga tgtgggtgct ctgtgctctg atcacagcct tgcttctggg ggtcacagag 360
 catgttctcg ccaacaatga tgtttctgtg gaccaccct ctaacaccgt gccctctggg 420
 agcaaccagg acctgggagc tggggccggg gaagacgccc ggtcggatga cagcagcagc 480
 cgcacatca atggatccga ctgcgatatg cacaccagc cgtggcaggc cgcgctgttg 540
 ctaaggccca accagctcta ctgcggggcg gtgttggtgc atccacagtg gctgctcacg 600
 gccgccact gcaggaagaa agttttcaga gtccgtctcg gccactact cctgtcacca 660
 gtttatgaat ctgggcagca gatgttccag ggggtcaa atccatcccc cctgggtac 720
 tcccaccctg gccactctaa cgacctcatg ctcatcaaac tgaacagaag aattcgtccc 780
 actaaagatg tcagacccat caacgtctcc tctcattgtc cctctgctgg gacaaagtgc 840
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cctgctgcag ggacagccct gacactcctt tcagaccctc attccttccc agagatgttg 1260
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gggcgggggt tgcgtctcaa tctccctggg gcactttcat cctcaagctc agggcccatc 1440
ccttctctgc agctctgacc caaatttagt cccagaaata aactgagaag tggaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1528

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<210> 30
<211> 293
<212> PRT
<213> Homo sapiens

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<400> 30

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Met Ala Thr Ala Arg Pro Pro Trp Met Trp Val Leu Cys Ala Leu Ile
1          5          10          15

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Thr Ala Leu Leu Leu Gly Val Thr Glu His Val Leu Ala Asn Asn Asp
20          25          30

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```

Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly Ser Asn Gln
35          40          45

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```

Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser Asp Asp Ser Ser
50          55          60

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Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met His Thr Gln Pro Trp
65          70          75          80

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Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln Leu Tyr Cys Gly Ala Val
85          90          95

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```

Leu Val His Pro Gln Trp Leu Leu Thr Ala Ala His Cys Arg Lys Lys
100         105         110

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```

Val Phe Arg Val Arg Leu Gly His Tyr Ser Leu Ser Pro Val Tyr Glu
115         120         125

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Ser Gly Gln Gln Met Phe Gln Gly Val Lys Ser Ile Pro His Pro Gly
130         135         140

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Tyr Ser His Pro Gly His Ser Asn Asp Leu Met Leu Ile Lys Leu Asn
145         150         155         160

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Arg Arg Ile Arg Pro Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser
165 170 175

His Cys Pro Ser Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr
180 185 190

Thr Lys Ser Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn
195 200 205

Ile Ser Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln
210 215 220

Ile Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser
225 230 235 240

Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu Gln
245 250 255

Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn Arg Pro
260 265 270

Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile Gln Glu Thr
275 280 285

Ile Gln Ala Asn Ser
290

<210> 31
<211> 19
<212> DNA
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<220>
<223> Oligonucleotide

<400> 31
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19

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 32
ctgggatgac tcaggagttg g

21

<210> 33
 <211> 636
 <212> DNA
 <213> Homo sapiens

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 agcattgctc acaccttcct ggagctaagc ttcgcctgcc ctggaggaag gtacgcaggc 180
 agtcgcccag ccccggttgc agggatggac cgcgaccagc agagggcaga aagtgcctgt 240
 gtccccatt ctcgatcccg gggccccaac ctcccatcgg ctccagtcctc cgcccaatct 300
 ctgccaggcc cggagctttc ccagaccctt caccacact ccaggctcac tccccgttcc 360
 tgggcctggg ccccccttgc acgagtccag ggccagccgt cctcgccttc tgcccgcccc 420
 cgtccttcgt tcctgggagc cggccctctc cgcggaccaa gcggccccga gcaggcgccg 480
 ccgcccgggg gactccgact cagccccgcg gacctacctc ggccgacagt cgggggttcc 540
 caagcggcca ctcccgccg gcgccgtccc ctggcggagc cgccgcgctc cctgccgtcc 600
 gcgcagtcctg gcctcgctcg gggccactcc tcgtag 636

<210> 34
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Thr Glu Ala Ala Ser Leu Val Pro Lys Arg Pro Arg Arg Leu Arg
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 Gly Ser His Lys Leu Arg Val Leu Ala Trp Pro Val Val Val Val Val
 20 25 30
 Asn Phe Val Trp Gln Cys Asn Gly Ser Ile Ala His Thr Phe Leu Glu
 35 40 45
 Leu Ser Phe Ala Cys Pro Gly Gly Arg Tyr Ala Gly Ser Arg Pro Ala
 50 55 60
 Pro Val Ala Gly Met Asp Arg Asp Gln Gln Arg Ala Glu Ser Ala Cys
 65 70 75 80
 Val Pro His Ser Arg Ser Arg Gly Pro Asn Leu Pro Ser Ala Gln Ser
 85 90 95

Pro Ala Gln Ser Leu Pro Gly Pro Glu Leu Ser Gln Thr Pro His Pro
 100 105 110

His Ser Arg Leu Thr Pro Arg Ser Trp Ala Trp Ala Pro Leu Ala Arg
 115 120 125

Val Gln Gly Gln Pro Ser Ser Pro Ser Ala Arg Pro Arg Pro Ser Phe
 130 135 140

Leu Gly Ala Gly Pro Leu Arg Gly Pro Ser Gly Pro Glu Gln Ala Pro
 145 150 155 160

Pro Pro Gly Gly Leu Arg Leu Ser Pro Arg Asp Leu Pro Arg Pro Thr
 165 170 175

Val Gly Gly Ser Gln Ala Ala Thr Pro Gly Arg Arg Arg Pro Leu Ala
 180 185 190

Glu Pro Pro Arg Ser Leu Pro Ser Ala Gln Ser Gly Leu Ala Arg Gly
 195 200 205

His Ser Ser
 210

<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 35
 tgctctcact gtggtcctca g 21

<210> 36
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 36
 tttgtaaagc tccagcgcta c 21

<210> 37
 <211> 969
 <212> DNA
 <213> Homo sapiens

<400> 37
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ctggggggcc tcatggcggt gccattcatc ctggccaagg acctgtgcct gcagcaggac 180
cccctgacac agagctacct catcagcacc attttctttg ctccagcatc tgcagtctcc 240
tgcaagctgc ccattcccca gggaggtacg tttgcttttg tggtaatttc tctggccatg 300
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cccagatgc tccagacagg gattctccag ccggaccagg ttgttcagat gctgctgacc 900
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cttcaataa 969

<210> 38
<211> 322
<212> PRT
<213> Homo sapiens

<400> 38

Met Lys Asp Cys Arg Asn Asn Gly Lys Asp Cys Gln Ser Ala Pro Ala
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Thr Arg Arg His Leu Phe Ser Glu Ala Ala Leu Pro Pro Tyr Arg Leu
20 25 30

Ser Gln Gly His Phe Leu Thr Ala Leu Gly Gly Leu Met Ala Val Pro
35 40 45

Phe Ile Leu Ala Lys Asp Leu Cys Leu Gln Gln Asp Pro Leu Thr Gln
50 55 60

Ser Tyr Leu Ile Ser Thr Ile Phe Phe Ala Pro Ala Ser Ala Cys Ser
 65 70 75 80
 Cys Lys Leu Pro Ile Pro Gln Gly Gly Thr Phe Ala Phe Val Val Ile
 85 90 95
 Ser Leu Ala Met Leu Ser Leu Pro Ser Trp Asn Cys Pro Glu Trp Thr
 100 105 110
 Leu Ser Ala Ser Gln Val Asn Thr Asn Phe Pro Glu Phe Thr Gln Lys
 115 120 125
 Trp Gln Lys Arg Ile Gln Glu Gly Ala Ile Met Val Thr Ser Cys Val
 130 135 140
 Arg Met Leu Val Gly Phe Ser Gly Leu Thr Gly Phe Leu Met Gly Phe
 145 150 155 160
 Ile Cys Ser Leu Ala Val Ala Pro Thr Asn Cys Leu Val Ala Leu Pro
 165 170 175
 Leu Leu Asp Ser Ala Gly Asn Asn Ala Gly Ile Gln Trp Gly Ile Ser
 180 185 190
 Ala Met Tyr Cys Phe Val Leu Arg Leu Arg Lys Asp Glu Leu Trp Pro
 195 200 205
 Phe Gly Ser Pro Arg Leu Arg Leu Pro Pro Ser Pro Pro Arg Asp Arg
 210 215 220
 Arg His Val Pro Thr Pro Val Ile Gly Gly Met Thr Leu Phe Gly Val
 225 230 235 240
 Ile Thr Ala Val Gly Ile Ser Asn Leu Gln Tyr Val Asp Met Asn Leu
 245 250 255
 Ser Arg Ser Leu Phe Ala Phe Gly Phe Ser Ile Tyr Cys Gly Leu Thr
 260 265 270
 Ile Pro Asn Arg Val Ser Lys Asn Pro Glu Met Leu Gln Thr Gly Ile
 275 280 285
 Leu Gln Pro Asp Gln Val Val Gln Met Leu Leu Thr Met Gly Met Phe
 290 295 300

Ile Ser Gly Phe Leu Gly Phe Leu Leu Asp Asn Thr Ile Pro Glu Leu
 305 310 315 320

Leu Gln

<210> 39
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 39
 atggcggtgc cattcatcct 20

<210> 40
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 40
 caggagggaa gggagagcat 20

<210> 41
 <211> 1679
 <212> DNA
 <213> Homo sapiens

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 ggccggcgctg ttgctctacc ggatcgcgcg gaggatgaag ccaacgcaca cgatgggtcaa 300
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 tccccactgc gagcagtaca acggcttcca ggagaacggc gactacaaca agccgatccc 420
 cgcccagtagc ttggagcacc tgaaccacgt ggtgagcagc gcgcccagcc tgcgcgaccc 480
 ttgcagccg cagcagtggg tgagcagcca agtcctgctg tgcaagaggt gcaaccacca 540
 ccagaccacc aagatcaagc agctggccgc cttcgctccc cgcgaggagg gcaggtatga 600
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ccaagcggct gtggagtact acatcaagca ccagaaccgc cagctgcgcg ccctgttgc 720
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<210> 42
 <211> 392
 <212> PRT
 <213> Homo sapiens

<400> 42

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Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu
 20 25 30

Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys
 35 40 45

Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
 50 55 60

Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
 65 70 75 80

Asp	Tyr	Asn	Lys	Pro	Ile	Pro	Ala	Gln	Tyr	Leu	Glu	His	Leu	Asn	His	85	90	95
Val	Val	Ser	Ser	Ala	Pro	Ser	Leu	Arg	Asp	Pro	Ser	Gln	Pro	Gln	Gln	100	105	110
Trp	Val	Ser	Ser	Gln	Val	Leu	Leu	Cys	Lys	Arg	Cys	Asn	His	His	Gln	115	120	125
Thr	Thr	Lys	Ile	Lys	Gln	Leu	Ala	Ala	Phe	Ala	Pro	Arg	Glu	Glu	Gly	130	135	140
Arg	Tyr	Asp	Glu	Glu	Val	Glu	Val	Tyr	Arg	His	His	Leu	Glu	Gln	Met	145	150	155
Tyr	Lys	Leu	Cys	Arg	Pro	Cys	Gln	Ala	Ala	Val	Glu	Tyr	Tyr	Ile	Lys	165	170	175
His	Gln	Asn	Arg	Gln	Leu	Arg	Ala	Leu	Leu	Leu	Ser	His	Gln	Phe	Lys	180	185	190
Arg	Arg	Glu	Ala	Asp	Gln	Thr	His	Ala	Gln	Asn	Phe	Ser	Ser	Ala	Val	195	200	205
Lys	Ser	Pro	Val	Gln	Val	Ile	Leu	Leu	Arg	Ala	Leu	Ala	Phe	Leu	Ala	210	215	220
Cys	Ala	Phe	Leu	Leu	Thr	Thr	Ala	Leu	Tyr	Gly	Ala	Ser	Gly	His	Phe	225	230	235
Ala	Pro	Gly	Thr	Thr	Val	Pro	Leu	Ala	Leu	Pro	Pro	Gly	Gly	Asn	Gly	245	250	255
Ser	Ala	Thr	Pro	Asp	Asn	Gly	Thr	Thr	Pro	Gly	Ala	Glu	Gly	Trp	Arg	260	265	270
Gln	Leu	Leu	Gly	Leu	Leu	Pro	Glu	His	Met	Ala	Glu	Lys	Leu	Cys	Glu	275	280	285
Ala	Trp	Ala	Phe	Gly	Gln	Ser	His	Gln	Thr	Gly	Val	Val	Ala	Leu	Gly	290	295	300
Leu	Leu	Thr	Cys	Leu	Leu	Ala	Met	Leu	Leu	Ala	Gly	Arg	Ile	Arg	Leu	305	310	315

Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
 325 330 335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
 340 345 350

Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
 355 360 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
 370 375 380

Pro Arg Arg Ser Glu Lys Gln Pro
 385 390

<210> 43
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 43
 ctacatcaag caccagaacc gcc 23

<210> 44
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 44
 ggacttcacg gcggaggag 19

<210> 45
 <211> 727
 <212> DNA
 <213> Homo sapiens

<400> 45
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 ggtgaaagga ctctggattg gttggcagtc tgcttttttt tttccaaggt gatcacttta 180
 ctgtagaaga aatgagggtta acagaaaaga gtgagggaga acaacaactc aagcccaaca 240

actctaattgc acccaatgaa gatcaagaag aagaaatcca acagtcagaa cagcatactc 300
cagcaaggca gcgaacacaa agagcagaca cacagccatc cagatgtcga ttgccttcac 360
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aatgagc 727

<210> 46
<211> 168
<212> PRT
<213> Homo sapiens

<400> 46

Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn
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Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser
20 25 30

Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln
35 40 45

Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser
50 55 60

Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp
65 70 75 80

Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu
85 90 95

Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu
100 105 110

Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe
115 120 125

Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu
130 135 140

Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile
 145 150 155 160

Ile Val Phe Ile Leu Ile Phe Phe
 165

<210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 47
 gctggtgaaa ggactctgga 20

<210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 48
 tcgctggatg ttgtaggtgt 20

<210> 49
 <211> 950
 <212> DNA
 <213> Homo sapiens

<400> 49
 gcgagcccga gcaggcagac gcgcggccgg cggctctgggg gcgcgccgcc tcccgggtccc 60
 caaaatgtga agcggggagg gcggagacgc agagacggcc cggccggggcg ccctcgccgc 120
 cctccggcag ccgcgccgct ccctccgctg cacgcccagg cctgagcagc gaggccaccg 180
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tccttctctca tctacctcag tgaggtcgag tggttctgcc ccccgctgcc 950

<210> 50
<211> 181
<212> PRT
<213> Homo sapiens

<400> 50

Met Ile Thr Val Asn Pro Asp Gly Lys Ile Met Val Arg Arg Cys Leu
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Val Thr Leu Arg Pro Phe Arg Leu Phe Val Leu Gly Ile Gly Phe Phe
20 25 30

Thr Leu Cys Phe Leu Met Thr Ser Leu Gly Gly Gln Phe Ser Ala Arg
35 40 45

Arg Leu Gly Asp Ser Pro Phe Thr Ile Arg Thr Glu Val Met Gly Gly
50 55 60

Pro Glu Ser Arg Gly Val Leu Arg Lys Met Ser Asp Leu Leu Glu Leu
65 70 75 80

Met Val Lys Arg Met Asp Ala Leu Ala Arg Leu Glu Asn Ser Ser Glu
85 90 95

Leu His Arg Ala Gly Gly Asp Leu His Phe Pro Ala Asp Arg Met Pro
100 105 110

Pro Gly Ala Gly Leu Met Glu Arg Ile Gln Ala Ile Ala Gln Asn Val
115 120 125

Ser Asp Ile Ala Val Lys Val Asp Gln Ile Leu Arg His Ser Leu Leu
130 135 140

Leu His Ser Lys Val Ser Glu Gly Arg Arg Asp Gln Cys Glu Ala Pro
145 150 155 160

Ser Asp Pro Lys Phe Pro Asp Cys Ser Gly Lys Val Ala Val Asp Ala
165 170 175

Cys Pro Leu Asp Leu
180

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 51
agatgcctgg tcaccctgag a 21

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<213> Homo sapiens

<400> 54

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His Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile
 35 40 45

Ser Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu
 50 55 60

Asn Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val
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Ser Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser
 85 90 95

Glu Gln Gly

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Ala	Val	Leu	Gln	Pro	Leu	Leu	Ala	Val	Phe	Arg	Pro	Pro	Leu	His	Asp
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Ala	Arg	Ile	Ile	Ala	Asp	Leu	Lys	Gln	Ser	Gly	Lys	Cys	Gly	Cys	Ile
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<210> 61
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<213> Homo sapiens

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<400> 62

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20          25          30

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Leu Leu Thr Trp Ser Leu Phe Thr Ala Trp Leu Arg Pro Pro Thr Leu
35          40          45

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Leu Gln Gly Pro Arg Thr Ser Pro Gln Gly Ser Pro Pro Arg Ser Pro
50          55          60

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Trp Gly Asp Cys Ala Glu Pro Ser Cys Leu Cys Glu Met Lys Ile Arg
65          70          75          80

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Arg Arg Arg His Glu Gly Pro Ala Trp Gly Gln Ser Gly Phe Leu Ala
85          90          95

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Gly Gly Leu His Leu Val Pro Ser Ser Leu Ser Leu Ala Ala Cys Gly
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Val Val Arg Met Lys Gly Leu Trp Gly Arg Gly Ala Gly Ile Arg Gly
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Arg

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<400> 66

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Ser Leu Phe His Phe Ile Val Phe Ser Pro Ser Phe Leu Ser Phe Ser
35 40 45

Leu Leu Leu Ser Phe Ser Ser Leu Leu Phe Pro Leu Val Phe Asn Phe
50 55 60

Asn Phe Asn Phe Trp Pro Ser Tyr Thr Ser Ile Cys Leu Ser Arg Lys
65 70 75 80

Leu Asn Ser Arg Gln Leu Ile Ile His Leu Ile Ser Ser Ala Lys Gln
85 90 95

Met Pro Ser Met Val Ser Phe Val Ile Arg Leu Leu Trp Asp Gln Asn
100 105 110

Val Ser Tyr Ser Ser Gly Lys Asn Glu Thr
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<400> 70

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 35 40 45

Ile Ile Tyr Gly Val Phe Ala Ile Leu Ser Gly Leu Val Val Leu Leu
 50 55 60

Leu Pro Glu Thr Arg Asn Gln Pro Leu Leu Asp Ser Ile Gln Asp Val
 65 70 75 80

Glu Asn Glu Gly Val Asn Ser Leu Ala Ala Pro Gln Arg Ser Ser Val
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Leu

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<210> 72
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Ile Ile Ile Ile Ile Ile Ile Phe Arg Trp Ser Leu Ala Leu Ser Leu
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Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala Arg Cys Lys Leu Arg Leu
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Glu Ala Tyr Ala Leu Pro Leu Val Val Lys Val Val Asp Asn Trp Ala
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Arg Lys Phe Trp Phe Lys Ser Ser Lys Ala Glu Asp Glu Tyr Glu His
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Glu Val Asp Trp Trp Ser Lys Leu Phe Trp Ala Thr Asp Glu His Lys
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Ser Leu Lys Tyr Lys Tyr Lys Asp Tyr His Thr Leu Lys Val Tyr Glu
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Gln Thr Phe Lys Leu Tyr Gln Glu Gln Pro Lys Leu Asp Ser Pro Val
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Pro Glu Ala Pro Lys Pro Pro Leu Gln Phe Leu Val Trp Pro Glu Arg
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Ile Leu Lys Leu Gly Lys Thr Glu Leu Gly Asn Arg Asp Met Tyr Gln
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Leu Phe Ser Pro Asp Asp Lys Ile Gly Thr Thr Val Ile Asp Leu Glu
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Tyr Cys Gln Ser Gly Pro Phe Arg Trp Arg Asp Gln Met Pro Pro Ser
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Phe Ser Pro Glu Glu Asp Ala Val Phe Tyr Asn Gly Lys Lys Phe Lys
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Lys Lys Glu Arg Leu Ala Leu Tyr Leu Leu His Thr Gln Gly Leu Val
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Pro Glu His Val Glu Thr Arg Thr Leu Tyr Ser His Ser Gln Pro Gly
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Leu Gly Pro Pro Gly Pro Gln Val Asn Ile Asn Pro Arg Lys Pro Lys
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Val Asp Asp Asn Leu Ser Arg Glu Lys Thr Ser Asp Ile Tyr Ile Lys
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Gly Trp Leu Tyr Gly Leu Glu Lys Asp Met Gln Lys Thr Asp Ile His
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Tyr His Ser Leu Thr Gly Glu Ala Asp Phe Asn Trp Arg Phe Ile Phe
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Thr Met Asp Tyr Leu Ala Ala Glu Arg Thr Cys Val Gln Ser Gln Lys
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Leu Gly Val Leu Glu Leu Asp Leu Ser Asp Met Pro Leu Pro Ala Arg
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His Ala Lys Gln Cys Ser Ile Arg Met Met Asp Ala Asp Pro Lys Trp
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690 695 700

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755 760 765

Asp Pro Asn Leu Lys Pro Thr Ile Asp His Glu Trp Lys Leu His Pro
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ccctccgccc cagcagaatt aaactttttt ctgtgtctga ggccctgctg acctgtgtgt	2940

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<210> 82
 <211> 684
 <212> PRT
 <213> Homo sapiens

<400> 82

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 1 5 10 15

Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu His
 20 25 30

Leu Asp Ser Asn Arg Leu Ala Glu Val Arg Gly Asp Gln Leu Arg Gly
 35 40 45

Leu Gly Asn Leu Arg His Leu Ile Leu Gly Asn Asn Gln Ile Arg Arg
 50 55 60

Val Glu Ser Ala Ala Phe Asp Ala Phe Leu Ser Thr Val Glu Asp Leu
 65 70 75 80

Asp Leu Ser Tyr Asn Asn Leu Glu Ala Leu Pro Trp Glu Ala Val Gly
 85 90 95

Gln Met Val Asn Leu Asn Thr Leu Thr Leu Asp His Asn Leu Ile Asp
 100 105 110

His Ile Ala Glu Gly Thr Phe Val Gln Leu His Lys Leu Val Arg Leu
 115 120 125

Asp Met Thr Ser Asn Arg Leu His Lys Leu Pro Pro Asp Gly Leu Phe
 130 135 140

Leu Arg Ser Gln Gly Thr Gly Pro Lys Pro Pro Thr Pro Leu Thr Val
 145 150 155 160

Ser Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu
 165 170 175

Arg Arg Leu Thr Arg Glu Asp Asp Leu Glu Thr Cys Ala Thr Pro Glu
 180 185 190

His Leu Thr Asp Arg Tyr Phe Trp Ser Ile Pro Glu Glu Glu Phe Leu
 195 200 205

Cys Glu Pro Pro Leu Ile Thr Arg Gln Ala Gly Gly Arg Ala Leu Val
 210 215 220

Val Glu Gly Gln Ala Val Ser Leu Arg Cys Arg Ala Val Gly Asp Pro
 225 230 235 240

Glu Pro Val Val His Trp Val Ala Pro Asp Gly Arg Leu Leu Gly Asn
 245 250 255

Ser Ser Arg Thr Arg Val Arg Gly Asp Gly Thr Leu Asp Val Thr Ile
 260 265 270

Thr Thr Leu Arg Asp Ser Gly Thr Phe Thr Cys Ile Ala Ser Asn Ala
 275 280 285

Ala Gly Glu Ala Thr Ala Pro Val Glu Val Cys Val Val Pro Leu Pro
 290 295 300

Leu Met Ala Pro Pro Pro Ala Ala Pro Pro Pro Leu Thr Glu Pro Gly
 305 310 315 320

Ser Ser Asp Ile Ala Thr Pro Gly Arg Pro Gly Ala Asn Asp Ser Ala
 325 330 335

Ala Glu Arg Arg Leu Val Ala Ala Glu Leu Thr Ser Asn Ser Val Leu
 340 345 350

Ile Arg Trp Pro Ala Gln Arg Pro Val Pro Gly Ile Arg Met Tyr Gln
 355 360 365

Val Gln Tyr Asn Ser Ser Val Asp Asp Ser Leu Val Tyr Arg Met Ile
 370 375 380

Pro Ser Thr Ser Gln Thr Phe Leu Val Asn Asp Leu Ala Ala Gly Arg
 385 390 395 400

Ala Tyr Asp Leu Cys Val Leu Ala Val Tyr Asp Asp Gly Ala Thr Ala
 405 410 415

Leu Pro Ala Thr Arg Val Val Gly Cys Val Gln Phe Thr Thr Ala Gly
 420 425 430

Asp Pro Ala Pro Cys Arg Pro Leu Arg Ala His Phe Leu Gly Gly Thr
 435 440 445

Met Ile Ile Ala Ile Gly Gly Val Ile Val Ala Ser Val Leu Val Phe
 450 455 460

Ile Val Leu Leu Met Ile Arg Tyr Lys Val Tyr Gly Asp Gly Asp Ser
 465 470 475 480

Arg Arg Val Lys Gly Ser Arg Ser Leu Pro Arg Val Ser His Val Cys
 485 490 495

Ser Gln Thr Asn Gly Ala Gly Thr Gly Ala Ala Gln Ala Pro Ala Leu
 500 505 510

Pro Ala Gln Asp His Tyr Glu Ala Leu Arg Glu Val Glu Ser Gln Ala
 515 520 525

Ala Pro Ala Val Ala Val Glu Ala Lys Ala Met Glu Ala Glu Thr Ala
 530 535 540

Ser Ala Glu Pro Glu Val Val Leu Gly Arg Ser Leu Gly Gly Ser Ala
 545 550 555 560

Thr Ser Leu Cys Leu Leu Pro Ser Glu Glu Thr Ser Gly Glu Glu Ser
 565 570 575

Arg Ala Ala Val Gly Pro Arg Arg Ser Arg Ser Gly Ala Leu Glu Pro
 580 585 590

Pro Thr Ser Ala Pro Pro Thr Leu Ala Leu Val Pro Gly Gly Ala Ala
 595 600 605

Ala Arg Pro Arg Pro Gln Gln Arg Tyr Ser Phe Asp Gly Asp Tyr Gly
 610 615 620

Ala Leu Phe Gln Ser His Ser Tyr Pro Arg Arg Ala Arg Arg Thr Lys
 625 630 635 640

Arg His Arg Ser Thr Pro His Leu Asp Gly Ala Gly Gly Gly Ala Ala
 645 650 655

Gly Glu Asp Gly Asp Leu Gly Leu Gly Ser Ala Arg Ala Cys Leu Ala
660 665 670

Phe Thr Ser Thr Glu Trp Met Leu Glu Ser Thr Val
675 680

<210> 83
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 83
cgaactccgt gctcatc 17

<210> 84
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 84
cgcacaaagtc gtaggca 17

<210> 85
<211> 2206
<212> DNA
<213> Homo sapiens

<400> 85
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acaccgaaga cgacaccagc catccggcca atcccgcccc gccgcgcccc gcaggccccgc 120
ccaactcctcg cttctccact tcccttctcg aagtgtccgg tcgcttctcg caggcggcgc 180
gcttgctggg tcacagttag gcggctccgc gcaggcgtag ccgggcgggc gaggagcggg 240
gaagctgact cagggtgtag gccgggggtc tgcggggtag gagcgcgagg ccggcctgag 300
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ttatgtttat ctcaattccc tgggtggtatt ggtgtctgct gggttttgcc agaataaaga 660

caccgtgttt	tcatttgtca	gttgattcgt	attttccagg	aagacattct	gagattacag	720
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agaaagttta	tgaagaactg	gctcacacca	tcacaaggca	aagtcccatg	acaggccatc	840
tgcaagctga	ggagcgagga	agccagcagt	ggctcagccg	gagtccaaca	gcctcaaacg	900
gaatccaaca	gttcaggctt	cagtctgtgg	ccaaatgccc	agagaccccc	gaaagctact	960
gggtgttagtc	ccagagccgg	aaggccaaag	aacctggagt	gtgatgtcca	agggcaggag	1020
gaatggacag	aagcatccag	catggggtaa	agacgaaagc	cagaagactc	agcaagctag	1080
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caccactgca	ctacagcttg	ggtgacagcg	cgagacaccg	tctcaaaaag	gataataatt	2040
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cataggctag	gaatgtaaga	tgtatgtgcc	tgtgtatata	cacacgtctg	tagctatgtc	2160
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<210> 86
 <211> 93
 <212> PRT
 <213> Homo sapiens
 <400> 86

Met Asp Arg Ser Ile Gln His Gly Val Lys Thr Lys Ala Arg Arg Leu
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Ser Lys Leu Ala Tyr Leu Leu Ser Ser Ala Cys Leu Val Leu Ala Ala
 20 25 30

Leu Ala Ala Gly Trp Arg Val Pro Thr Pro Thr Glu Gly Gly Ser Ser
 35 40 45

Ser Pro Ser Pro Leu Thr Gln Ile Ser Val Ser Leu Gly Ala Pro Ser
 50 55 60

His Gln Lys Gln Tyr Gln Pro Ser Ser His Pro Ser Val His His His
 65 70 75 80

Asn His Cys Leu Ile His Glu Thr Ser Ala Asp Pro Pro
 85 90

<210> 87
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 87
 aaactacgtg tggccaggat c 21

<210> 88
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 88
 cgacatgagg actcaggaca c 21

<210> 89
 <211> 455
 <212> DNA
 <213> Homo sapiens

<400> 89
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 catgagaaca cggctctttga tggggataat tactctgaat ctaccaggct gattaagcca 120
 cagcagatca gcaggtgaga attcaactgt ccagatagaa aggtggacat ggaaaaattg 180

ggctttgcaa atgggcaccc aattcttgcc ttcttggtct ccagatcacc cttcctatac 240
 cgccactctg gagaaagaag tacagaacgc taacaaggat ggcttggagt tgcagtggtc 300
 acctcagatc ttaaggtcac tttggagatg gaaccctgt gactaggaat ggcagaagag 360
 aaaggtagaa agagattgag tcctggggat gtggcagagc accatcctag ccccgtagtg 420
 cgtacttctg gacttccttt aaattgagag aaaca 455

<210> 90
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 90

Cys Phe Ser Gln Phe Lys Gly Ser Pro Glu Val Arg Ser Thr Gly Leu
 1 5 10 15

Gly Trp Cys Ser Ala Thr Ser Pro Gly Leu Asn Leu Phe Leu Pro Phe
 20 25 30

Ser Ser Ala Ile Pro Ser His Arg Gly Ser Ile Ser Lys Val Thr Leu
 35 40 45

Arg Ser Glu Val Thr Thr Ala Thr Pro Ser His Pro Cys
 50 55 60

<210> 91
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 91
 gaacacggtc tttgatgggg 20

<210> 92
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 92
 gccatccttg ttagcgttct g 21

<210> 93
 <211> 1230

<212> DNA
<213> Homo sapiens

<400> 93
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taatattaaa aataaacgga gaaaaaaaaat cctgttttcgc taacggctgg tggtagcagg 120
ttgagtaccg ggagggctgc aagaccgtga ttgatgggga ggactgcgca gaccctggcg 180
agggtgagcc cctccccgga ggcgcctgtg gaatgtccag ggctctggtc cgctcctcgg 240
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tccacgcata aataaagatt taacgaactg 1230

<210> 94
<211> 159
<212> PRT
<213> Homo sapiens

<400> 94
Met Ala Asp Val Pro Gly Ala Gln Arg Ala Val Pro Gly Asp Gly Pro
1 5 10 15
Glu Pro Arg Asp Pro Leu Asp Cys Trp Ala Cys Ala Val Leu Val Thr
20 25 30

Ala Gln Asn Leu Leu Val Ala Ala Phe Asn Leu Leu Leu Leu Val Leu
 35 40 45

Val Leu Gly Thr Ile Leu Leu Pro Ala Val Thr Met Leu Gly Phe Gly
 50 55 60

Phe Leu Cys His Ser Gln Phe Leu Arg Ser Gln Ala Pro Pro Cys Thr
 65 70 75 80

Ala His Leu Arg Asp Pro Gly Phe Thr Ala Leu Leu Val Thr Gly Phe
 85 90 95

Leu Leu Leu Val Pro Leu Leu Val Leu Ala Leu Ala Ser Tyr Arg Arg
 100 105 110

Leu Cys Leu Arg Leu Arg Leu Ala Asp Cys Leu Val Pro Tyr Ser Arg
 115 120 125

Ala Leu Tyr Arg Arg Arg Arg Ala Pro Gln Pro Arg Gln Ile Arg Ala
 130 135 140

Ser Pro Gly Ser Gln Ala Val Pro Thr Ser Gly Lys Val Trp Val
 145 150 155

<210> 95
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 95
 ttctctctgcc actctcagtt c 21

<210> 96
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 96
 cgataaaggg ctcggctgta g 21

<210> 97
 <211> 1020

<212> DNA
<213> Homo sapiens

<400> 97
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cctcccaagc cagggaccat ggaggaggag gaggaggatg atgactatga gaactcaaca 120
cctccctaca aggaccttcc tccaagcca gggaccatgg aggaggagga ggaggatgat 180
gactatgaga actcaacacc tccctacaag gaccttcctc ccaagccagg ttcaagtgt 240
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cggaacatga caggcctgga cctgcgcgt gtcacctgtc cacctcctca actggctgtg 360
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gaggaaccca ataacatcca cgatgaggac tgtgctacca tgaacaaagg tggcacctgg 960
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<210> 98
<211> 339
<212> PRT
<213> Homo sapiens

<400> 98
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Tyr Lys Asp Leu Pro Pro Lys Pro Gly Thr Met Glu Glu Glu Glu Glu
20 25 30
Asp Asp Asp Tyr Glu Asn Ser Thr Pro Pro Tyr Lys Asp Leu Pro Pro
35 40 45
Lys Pro Gly Thr Met Glu Glu Glu Glu Glu Asp Asp Asp Tyr Glu Asn
50 55 60

Ser Thr Pro Pro Tyr Lys Asp Leu Pro Pro Lys Pro Gly Ser Ser Ala
 65 70 75 80
 Pro Pro Arg Pro Pro Arg Ala Ala Lys Glu Thr Glu Lys Pro Pro Leu
 85 90 95
 Pro Cys Lys Pro Arg Asn Met Thr Gly Leu Asp Leu Ala Ala Val Thr
 100 105 110
 Cys Pro Pro Pro Gln Leu Ala Val Asn Leu Glu Pro Ser Pro Leu Gln
 115 120 125
 Pro Ser Leu Ala Ala Thr Pro Val Pro Trp Leu Asn Gln Arg Ser Gly
 130 135 140
 Gly Pro Gly Cys Cys Gln Lys Arg Trp Met Val Tyr Leu Cys Leu Leu
 145 150 155 160
 Val Val Thr Ser Leu Phe Leu Gly Cys Leu Gly Leu Thr Val Thr Leu
 165 170 175
 Ile Lys Leu Thr Gly Met Ala Gly Leu Ala Gly Leu Lys His Asp Ile
 180 185 190
 Ala Arg Val Arg Ala Asp Thr Asn Gln Ser Leu Val Glu Leu Trp Gly
 195 200 205
 Leu Leu Asp Cys Arg Arg Ile Thr Cys Pro Glu Gly Trp Leu Pro Phe
 210 215 220
 Glu Gly Lys Cys Tyr Tyr Phe Ser Pro Ser Thr Lys Ser Trp Asp Glu
 225 230 235 240
 Ala Arg Met Phe Cys Gln Glu Asn Tyr Ser His Leu Val Ile Ile Asn
 245 250 255
 Ser Phe Ala Glu His Asn Phe Val Ala Lys Ala His Gly Ser Pro Arg
 260 265 270
 Val Tyr Trp Leu Gly Leu Asn Asp Arg Ala Gln Glu Gly Asp Trp Arg
 275 280 285
 Trp Leu Asp Gly Ser Pro Val Thr Leu Arg Gln Pro Glu Glu Pro Asn
 290 295 300

Asn Ile His Asp Glu Asp Cys Ala Thr Met Asn Lys Gly Gly Thr Trp
 305 310 315 320

Asn Asp Leu Ser Cys Tyr Lys Thr Thr Tyr Trp Ile Cys Glu Arg Lys
 325 330 335

Cys Ser Cys

<210> 99
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 99
 atagctttgc tgagcacctt c 21

<210> 100
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 100
 aagagacact cagatatgga c 21

<210> 101
 <211> 1680
 <212> DNA
 <213> Homo sapiens

<400> 101
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 ctgcggattt tatatggtgt gctcttecta ctgatttacc tggcagccct aatgagtaac 120
 cttctcatca ttactctcat taccctggac gtaaagctcc aaacacccat gtacttcttc 180
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 ctgatcaaag ctgtccacgt cctgaacact gtggtgactc cagttttaaa ccccttcatc 1620
 tatacgcttc gtaataagga agtaagagag actctgctga agaaatggaa gggaaaataa 1680

<210> 102
 <211> 559
 <212> PRT
 <213> Homo sapiens

<400> 102

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser
 1 5 10 15

Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile
 20 25 30

Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr
 35 40 45

Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu
 50 55 60

Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile
 65 70 75 80

Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala
 85 90 95

Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile
 100 105 110

Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu
 115 120 125

Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser
 130 135 140

Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly
 145 150 155 160

Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe
 165 170 175

Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met
 180 185 190

Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys
 195 200 205

Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu
 210 215 220

Lys Ile Pro Thr Thr Lys Gly Leu Cys Asp Trp Val Lys Gly Leu Ser
 225 230 235 240

Ala Gly Thr Leu Phe Ser Gly Phe Ser Thr Thr Met Asp Thr Gly Asn
 245 250 255

Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly Phe Pro Gly Ser Gln
 260 265 270

Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu Val Met Tyr Ile Leu
 275 280 285

Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu Val Ser Thr Ser His
 290 295 300

Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
 305 310 315 320

Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys Ala Leu Ala Ile Leu
 325 330 335

Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser Cys Leu Leu Gln Met
 340 345 350

Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr Phe Leu Leu Ala Ala
 355 360 365

Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly
 370 375 380

Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu Ala Leu Gly Ser Trp
 385 390 395 400

Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr Ala Leu Ile Ser Gly
 405 410 415

Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His Phe Phe Cys Asp Ile
 420 425 430

Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr Gln Ala Val Glu Leu
 435 440 445

Val Ala Phe Val Ile Ala Val Val Val Ile Leu Ser Ser Cys Leu Ile
 450 455 460

Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro
 465 470 475 480

Ser Ala Ser Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu
 485 490 495

Thr Val Val Leu Ile Trp Tyr Gly Ser Thr Val Phe Leu His Val Arg
 500 505 510

Thr Ser Ile Lys Asp Ala Leu Asp Leu Ile Lys Ala Val His Val Leu
 515 520 525

Asn Thr Val Val Thr Pro Val Leu Asn Pro Phe Ile Tyr Thr Leu Arg
 530 535 540

Asn Lys Glu Val Arg Glu Thr Leu Leu Lys Lys Trp Lys Gly Lys
 545 550 555

<210> 103
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<220>
 <223> Oligonucleotide

<400> 103
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<210> 104
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 <212> DNA
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<220>
 <223> Oligonucleotide

<400> 104
 tgttgcctgt gtccattgtg 20

<210> 105
 <211> 499
 <212> DNA
 <213> Homo sapiens

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 ttgcatccgg aaccaggact gcgagactgg ctgctgccaa cgtgctccag acaattgcga 240
 gtgcgactgc gcggagaagg ggtccgaggg cagtctgtgt caaacgcagg tggtcttttg 300
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<210> 106
 <211> 121
 <212> PRT

<213> Homo sapiens

<400> 106

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Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu
20 25 30

Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly
35 40 45

Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys
50 55 60

Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr
65 70 75 80

Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn
85 90 95

Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg
100 105 110

Gln Lys Leu Ala Lys Lys Met Phe Phe
115 120

<210> 107

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide

<400> 107

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17

<210> 108

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide

<400> 108

ggagggagca ctagaagaac

20

<210> 109
 <211> 659
 <212> DNA
 <213> Homo sapiens

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 aaaataactc tgtcacttct gttatatggt atcattgctt gtaattatct atttacttat 540
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 ttggtagtca ctcataaatc gtttattgca ttactaacta aataaaaaag ttgaccttg 659

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 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 110

Met Lys Val Ile Ala Glu Thr Phe Tyr Trp Leu Pro Gly Cys Arg His
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 20 25 30

Ser Arg Ser His Phe Tyr His Leu Gln Gln Ser Ser Ser Val Ser Ser
 35 40 45

Pro Gly Leu Asp Phe Ile Leu Gln Ser Asp Ser Met Cys Leu Pro Tyr
 50 55 60

Phe Lys Asp Ser Leu Leu Phe Leu Ala Tyr Arg Glu Gln Thr Leu Phe
 65 70 75 80

Phe Ala Phe Leu Val Cys Ser Arg Phe Ser Lys Ile Thr Leu Ser Leu
 85 90 95

Leu Leu Tyr Gly Ile Ile Ala Cys Asn Tyr Leu Phe Thr Tyr Leu Ser
100 105 110

Leu Asp Trp Thr Leu Tyr Arg Gln Ala Ile Thr Asn Tyr Leu Ser Val
115 120 125

Trp His Leu Val Val Thr His Lys Ser Phe Ile Ala Leu Leu Thr Lys
130 135 140

<210> 111
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 111
atcctggcga atgaaacaag agaat 25

<210> 112
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 112
gcaaccagta aaatgtctca gcaatg 26

<210> 113
<211> 831
<212> DNA
<213> Homo sapiens

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gccttccacc tcaactgtgtt cattgtccat tatggctgtg cttccattgc ctacctcatg 780
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<210> 114
<211> 276
<212> PRT
<213> Homo sapiens

<400> 114

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20 25 30

Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile
35 40 45

Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50 55 60

Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln
65 70 75 80

Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly
85 90 95

Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys
100 105 110

Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn
115 120 125

Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu
130 135 140

Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val
145 150 155 160

Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe
165 170 175

Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr
180 185 190

Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val
195 200 205

Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val
210 215 220

Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys
225 230 235 240

Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile
245 250 255

Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu
260 265 270

Leu Ser Val Thr
275

<210> 115
<211> 18
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<220>
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<400> 115
cttcgtaacc cagaccca 18

<210> 116
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 116
cttgctcgta atgaccct 18

<210> 117
<211> 1233
<212> DNA
<213> Homo sapiens

<400> 117


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<210> 118
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<212> PRT
<213> Homo sapiens

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<400> 118

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Met Ser Ile Ser Ser Leu Leu Asn Asn Thr Thr Phe Ser Thr Gly Phe
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His Lys Phe Arg Gly Lys Ser Met Asn Ile His Glu Val Thr Ile Thr
          20          25          30

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Thr Leu Thr Thr Thr Thr Ile Ile Ser Thr Ile Phe Thr Leu Leu Ile
          35          40          45

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Arg Lys Leu Pro Pro Arg Leu Pro Glu Val Thr Gln Lys Cys Ile Ser
 50 55 60

Pro Arg Val Ser Cys Ala Asn Ile Val Ser Tyr Gly Thr Leu Gly Ser
 65 70 75 80

Tyr Pro Asp Pro Gln Leu Leu Glu Ser Cys
 85 90

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 <211> 19
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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 119
 caccaccacct tcgtctttg 19

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 120
 gttttacctt tgatctccac tttc 24

<210> 121
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 <212> DNA
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<210> 122
 <211> 1343
 <212> PRT
 <213> Homo sapiens

<400> 122

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Asn Ala Pro Ser Ser Thr Pro Trp Val Leu Asp Ile Phe Leu Thr Leu
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Val Phe Ala Leu Gly Phe Phe Phe Leu Leu Leu Pro Tyr Leu Ser Tyr
35 40 45

Phe His Cys Asp Asp Pro Pro Ser Pro Ser Pro Gly Lys Arg Lys Cys
50 55 60

Pro Val Gly Arg Arg Arg Arg Pro Arg Gly Arg Met Lys Asn His Ser
65 70 75 80

Leu Arg Ala Gly Arg Glu Cys Pro Arg Gly Leu Glu Glu Thr Ser Asp
85 90 95

Leu Leu Ser Gln Leu Gln Ser Leu Leu Gly Pro His Leu Asp Lys Gly
100 105 110

Asp Phe Gly Gln Leu Ser Gly Pro Asp Pro Pro Gly Glu Val Gly Glu
115 120 125

Arg Ala Pro Asp Gly Ala Ser Gln Ser Ser His Glu Pro Met Glu Asp
130 135 140

Ala Ala Pro Ile Leu Ser Pro Leu Ala Ser Pro Asp Pro Gln Ala Lys
145 150 155 160

His Pro Gln Asp Leu Ala Ser Thr Pro Ser Pro Gly Pro Met Thr Thr
165 170 175

Ser Val Ser Ser Leu Ser Ala Ser Gln Pro Pro Glu Pro Ser Leu Pro
180 185 190

Leu Glu His Pro Ser Pro Glu Pro Pro Ala Leu Phe Pro His Pro Pro
 195 200 205

His Thr Pro Asp Pro Leu Ala Cys Ser Pro Pro Pro Pro Lys Gly Phe
 210 215 220

Thr Ala Pro Pro Leu Arg Asp Ser Thr Leu Ile Thr Pro Ser His Cys
 225 230 235 240

Asp Ser Val Ala Leu Pro Leu Gly Thr Val Pro Gln Ser Leu Ser Pro
 245 250 255

His Glu Asp Leu Val Ala Ser Val Pro Ala Ile Ser Gly Leu Gly Gly
 260 265 270

Ser Asn Ser His Val Ser Ala Ser Ser Arg Trp Gln Glu Thr Ala Arg
 275 280 285

Thr Ser Cys Ala Phe Asn Ser Ser Val Gln Gln Asp Pro Leu Ser Arg
 290 295 300

His Pro Pro Glu Thr Cys Gln Met Glu Ala Gly Ser Leu Phe Leu Leu
 305 310 315 320

Ser Ser Asp Gly Gln Asn Val Val Gly Ile Gln Val Thr Glu Thr Ala
 325 330 335

Lys Val Asn Ile Trp Glu Glu Lys Glu Asn Val Gly Ser Phe Thr Asn
 340 345 350

Gln Met Thr Pro Glu Lys His Leu Asn Ser Leu Gly Asn Leu Ala Lys
 355 360 365

Ser Leu Asp Ala Glu Gln Asp Thr Thr Asn Pro Lys Pro Phe Trp Asn
 370 375 380

Met Gly Glu Asn Ser Lys Gln Leu Pro Gly Pro Gln Lys Cys Ser Asp
 385 390 395 400

Pro Arg Leu Leu Gln Glu Ser Phe Trp Lys Asn Tyr Ser Gln Leu Phe
 405 410 415

Trp Gly Leu Pro Ser Leu His Ser Glu Ser Leu Val Ala Asn Ala Trp
 420 425 430

Val Thr Asp Arg Ser Tyr Thr Leu Gln Ser Pro Pro Phe Leu Phe Asn
435 440 445

Glu Met Ser Asn Val Cys Pro Ile Gln Arg Glu Thr Thr Met Ser Pro
450 455 460

Leu Leu Phe Gln Ala Gln Pro Leu Ser His Arg Gln Pro Phe Ile Ser
465 470 475 480

Ser Thr Pro Gln Phe Leu Pro Thr Pro Met Ala Gln Ala Glu Ala Gln
485 490 495

Ala His Leu Gln Ser Ser Phe Pro Val Leu Ser Pro Ala Phe Pro Ser
500 505 510

Leu Ile Lys Asn Thr Gly Val Ala Cys Pro Ala Ser Gln Asn Lys Val
515 520 525

Gln Ala Leu Ser Leu Pro Glu Thr Gln His Pro Glu Trp Pro Leu Leu
530 535 540

Arg Lys Gln Leu Glu Gly Arg Leu Ala Leu Pro Ser Arg Val Gln Lys
545 550 555 560

Ser Gln Asp Val Phe Ser Val Ser Thr Pro Asn Leu Pro Gln Glu Ser
565 570 575

Leu Thr Ser Ile Leu Pro Glu Asn Phe Pro Val Ser Pro Glu Leu Arg
580 585 590

Arg Gln Leu Glu Gln His Ile Lys Lys Trp Ile Ile Gln His Trp Gly
595 600 605

Asn Leu Gly Arg Ile Gln Glu Ser Leu Asp Leu Met Gln Leu Arg Asp
610 615 620

Glu Ser Pro Gly Thr Ser Gln Ala Lys Gly Lys Pro Ser Pro Trp Gln
625 630 635 640

Ser Ser Thr Ser Thr Gly Glu Ser Ser Lys Glu Ala Gln Lys Val Lys
645 650 655

Phe Gln Leu Glu Arg Asp Leu Cys Pro His Leu Gly Gln Ile Leu Gly
660 665 670

Glu Thr Pro Gln Asn Leu Ser Arg Asp Met Lys Ser Phe Pro Arg Lys
675 680 685

Val Leu Gly Val Thr Ser Glu Glu Ser Glu Arg Asn Leu Arg Lys Pro
690 695 700

Leu Arg Ser Asp Ser Gly Ser Asp Leu Leu Arg Cys Thr Glu Arg Thr
705 710 715 720

His Ile Glu Asn Ile Leu Lys Ala His Met Gly Arg Asn Leu Gly Gln
725 730 735

Thr Asn Glu Gly Leu Ile Pro Val Arg Val Arg Arg Ser Trp Leu Ala
740 745 750

Val Asn Gln Ala Leu Pro Val Ser Asn Thr His Val Lys Thr Ser Asn
755 760 765

Leu Ala Ala Pro Lys Ser Gly Lys Ala Cys Val Asn Thr Ala Gln Val
770 775 780

Leu Ser Phe Leu Glu Pro Cys Thr Gln Gln Gly Leu Gly Ala His Ile
785 790 795 800

Val Arg Phe Trp Ala Lys His Arg Trp Gly Leu Pro Leu Arg Val Leu
805 810 815

Lys Pro Ile Gln Cys Phe Lys Leu Glu Lys Val Ser Ser Leu Ser Leu
820 825 830

Thr Gln Leu Ala Gly Pro Ser Ser Ala Thr Cys Glu Ser Gly Ala Gly
835 840 845

Ser Glu Val Glu Val Asp Met Phe Leu Arg Lys Pro Pro Met Ala Ser
850 855 860

Leu Arg Lys Gln Val Leu Thr Lys Ala Ser Asp His Met Pro Glu Ser
865 870 875 880

Leu Leu Ala Ser Ser Pro Ala Trp Lys Gln Phe Gln Arg Ala Pro Arg
885 890 895

Gly Ile Pro Ser Trp Asn Asp His Gly Pro Leu Lys Pro Pro Pro Ala
900 905 910

Gly Gln Glu Gly Arg Trp Pro Ser Lys Pro Leu Thr Tyr Ser Leu Thr
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Gly Ser Thr Gln Gln Ser Arg Ser Leu Gly Ala Gln Ser Ser Lys Ala
 930 935 940

Gly Glu Thr Arg Glu Ala Val Pro Gln Cys Arg Val Pro Leu Glu Thr
 945 950 955 960

Cys Met Leu Ala Asn Leu Gln Ala Thr Ser Glu Asp Val His Gly Phe
 965 970 975

Glu Ala Pro Gly Thr Ser Lys Ser Ser Leu His Pro Arg Val Ser Val
 980 985 990

Ser Gln Asp Pro Arg Lys Leu Cys Leu Met Glu Glu Val Val Ser Glu
 995 1000 1005

Phe Glu Pro Gly Met Ala Thr Lys Ser Glu Thr Gln Pro Gln Val
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Cys Ala Ala Val Val Leu Leu Pro Asp Gly Gln Ala Ser Val Val
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Pro His Ala Ser Glu Asn Leu Val Ser Gln Val Pro Gln Gly His
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Leu Gln Ser Met Pro Thr Gly Asn Met Arg Ala Ser Gln Glu Leu
 1055 1060 1065

His Asp Leu Met Ala Ala Arg Arg Ser Lys Leu Val Gln Glu Glu
 1070 1075 1080

Pro Arg Asn Pro Asn Cys Gln Gly Ser Cys Lys Ser Gln Arg Pro
 1085 1090 1095

Met Phe Pro Pro Ile His Lys Ser Glu Lys Ser Arg Lys Pro Asn
 1100 1105 1110

Leu Glu Lys His Glu Glu Arg Leu Glu Gly Leu Arg Thr Pro Gln
 1115 1120 1125

Leu Thr Pro Val Arg Lys Thr Glu Asp Thr His Gln Asp Glu Gly
 1130 1135 1140

Val	Gln	Leu	Leu	Pro	Ser	Lys	Lys	Gln	Pro	Pro	Ser	Val	Ser	His
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Phe	Gly	Glu	Asn	Ile	Lys	Gln	Phe	Phe	Gln	Trp	Ile	Phe	Ser	Lys
1160						1165					1170			
Lys	Lys	Ser	Lys	Pro	Ala	Pro	Val	Thr	Ala	Glu	Ser	Gln	Lys	Thr
1175						1180					1185			
Val	Lys	Asn	Arg	Ser	Cys	Val	Tyr	Ser	Ser	Ser	Ala	Glu	Ala	Gln
1190						1195					1200			
Gly	Leu	Met	Thr	Ala	Val	Gly	Gln	Met	Leu	Asp	Lys	Lys	Met	Ser
1205						1210					1215			
Leu	Cys	His	Ala	His	His	Ala	Ser	Lys	Val	Asn	Gln	His	Lys	Gln
1220						1225					1230			
Lys	Phe	Gln	Ala	Pro	Val	Cys	Gly	Phe	Pro	Cys	Asn	His	Arg	His
1235						1240					1245			
Leu	Phe	Tyr	Ser	Glu	His	Gly	Arg	Ile	Leu	Ser	Tyr	Ala	Ala	Ser
1250						1255					1260			
Ser	Gln	Gln	Ala	Thr	Leu	Lys	Ser	Gln	Gly	Cys	Pro	Asn	Arg	Asp
1265						1270					1275			
Arg	Gln	Ile	Arg	Asn	Gln	Gln	Pro	Leu	Lys	Ser	Val	Arg	Cys	Asn
1280						1285					1290			
Asn	Glu	Gln	Trp	Gly	Leu	Arg	His	Pro	Gln	Ile	Leu	His	Pro	Lys
1295						1300					1305			
Lys	Ala	Val	Ser	Pro	Val	Ser	Pro	Pro	Gln	His	Trp	Pro	Lys	Thr
1310						1315					1320			
Ser	Gly	Ala	Ser	Ser	His	His	His	His	Cys	Pro	Arg	His	Cys	Leu
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 gtattgcaca tttgtctggc tttctgtagc cttctgcttt tcagcgttgc cacacaatgt 240
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 <213> Homo sapiens

<400> 126

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Arg Arg Arg Glu Ile Ala His Val His Ala Glu Lys Gly Gln Ser Asp
 35 40 45

Lys Met Asn Thr Asp Asp Leu Glu Asn Ser Ser Val Thr Ser Lys Gln
 50 55 60

Thr Pro Gln Leu Val Val Ser Glu Asp Pro Met Met Met Ser Ala Val
 65 70 75 80

Pro Ser Ala Thr Ser Leu Asn Lys Ala Phe Ser Ile Asn Lys Glu Thr
 85 90 95

Gln Pro Gly Gln Ala Gly Leu Met Gln Thr Glu Arg Pro Gly Val Ser
 100 105 110

Thr Pro Thr Glu Ser Gly Val Pro Ser Ala Glu Glu Val Phe Gly Ser
 115 120 125

Ser Gln Pro Glu Arg Ile Ser Pro Glu Ser Gly Leu Ala Lys Ala Met
 130 135 140

Leu Thr Ile Ala Ile Thr Ala Thr Pro Ser Leu Thr Val Asp Glu Lys
 145 150 155 160

Glu Glu Leu Leu Thr Ser Thr Asn Phe Gln Pro Ile Val Glu Glu Ile
165 170 175

Thr Glu Thr Thr Lys Gly Phe Leu Lys Tyr Met Asp Asn Gln Ser Phe
180 185 190

Ala Thr Glu Ser Gln Glu Gly Val Gly Leu Gly His Ser Pro Ser Ser
195 200 205

Tyr Val Asn Thr Lys Glu Met Leu Thr Thr Asn Pro Lys Thr Glu Lys
210 215 220

Phe Glu Ala Asp Thr Asp His Arg Thr Thr Ser Phe Pro Gly Ala Glu
225 230 235 240

Ser Thr Ala Gly Ser Glu Pro Gly Ser Leu Thr Pro Asp Lys Glu Lys
245 250 255

Pro Ser Gln Met Thr Ala Asp Asn Thr Gln Ala Ala Ala Thr Lys Gln
260 265 270

Pro Leu Glu Thr Ser Glu Tyr Thr Leu Ser Val Glu Pro Glu Thr Asp
275 280 285

Ser Leu Leu Gly Ala Pro Glu Val Thr Val Ser Val Ser Thr Ala Val
290 295 300

Pro Ala Ala Ser Ala Leu Ser Asp Glu Trp Asp Asp Thr Lys Leu Glu
305 310 315 320

Ser Val Ser Arg Ile Arg Thr Pro Lys Leu Gly Asp Asn Glu Glu Thr
325 330 335

Gln Val Arg Thr Glu Met Ser Gln Thr Ala Gln Val Ser His Glu Gly
340 345 350

Met Glu Gly Gly Gln Pro Trp Thr Glu Ala Ala Gln Val Ala Leu Gly
355 360 365

Leu Pro Glu Gly Glu Thr His Thr Gly Thr Ala Leu Leu Ile Ala His
370 375 380

Gly Asn Glu Arg Ser Pro Ala Phe Thr Asp Gln Ser Ser Phe Thr Pro
385 390 395 400

Thr Ser Leu Met Glu Asp Met Lys Val Ser Ile Val Asn Leu Leu Gln
405 410 415

Ser Thr Gly Asp Phe Thr Glu Ser Thr Lys Glu Asn Asp Ala Leu Phe
420 425 430

Phe Leu Glu Thr Thr Val Ser Val Ser Val Tyr Glu Ser Glu Ala Asp
435 440 445

Gln Leu Leu Gly Asn Thr Met Lys Asp Ile Ile Thr Gln Glu Met Thr
450 455 460

Thr Ala Val Gln Glu Pro Asp Ala Thr Leu Ser Met Val Thr Gln Glu
465 470 475 480

Gln Val Ala Thr Leu Glu Leu Ile Arg Asp Ser Gly Lys Thr Glu Glu
485 490 495

Glu Lys Glu Asp Pro Ser Pro Val Ser Asp Val Pro Gly Val Thr Gln
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Leu Ser Arg Arg Trp Glu Pro Leu Ala Thr Thr Ile Ser Thr Thr Val
515 520 525

Val Pro Leu Ser Phe Glu Val Thr Pro Thr Val Glu Glu Gln Met Asp
530 535 540

Thr Val Thr Gly Pro Asn Glu Glu Phe Thr Pro Val Leu Gly Ser Pro
545 550 555 560

Val Thr Pro Pro Gly Ile Met Val Gly Glu Pro Ser Ile Ser Pro Ala
565 570 575

Leu Pro Ala Leu Glu Ala Ser Ser Glu Arg Arg Thr Val Val Pro Ser
580 585 590

Ile Thr Arg Val Asn Thr Ala Ala Ser Tyr Gly Leu Asp Gln Leu Glu
595 600 605

Ser Glu Glu Gly Gln Glu Asp Glu Asp Glu Glu Asp Glu Glu Asp Glu
610 615 620

Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Glu Glu Asp Lys Asp Ala
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Asp Ser Leu Asp Glu Gly Leu Asp Gly Asp Thr Glu Leu Pro Gly Phe
645 650 655

Thr Leu Pro Gly Ile Thr Ser Gln Glu Pro Gly Leu Glu Glu Gly Asn
660 665 670

Met Asp Leu Leu Glu Gly Ala Thr Tyr Gln Val Pro Asp Ala Leu Glu
675 680 685

Trp Glu Gln Gln Asn Gln Gly Leu Val Arg Ser Trp Met Glu Lys Leu
690 695 700

Lys Asp Lys Ala Gly Tyr Met Ser Gly Met Leu Val Pro Val Gly Val
705 710 715 720

Gly Ile Ala Gly Ala Leu Phe Ile Leu Gly Ala Leu Tyr Ser Ile Lys
725 730 735

Val Met Asn Arg Arg Arg Arg Asn Gly Phe Lys Arg His Lys Arg Lys
740 745 750

Gln Arg Glu Phe Asn Ser Met Gln Asp Arg Val Met Leu Leu Ala Asp
755 760 765

Ser Ser Glu Asp Glu Phe
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18

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tcaagataac ctggtggctc tgtgccattc cctacagtat tctcatcttc gtctatgatg	3480
aaatcagaaa actcctcatc cgtcagcacc cggatggctg ggtggaaagg gagacgtact	3540
actaaactca gcagatgaag agcttcatgt gacacagggg tgttgtgaga gctgggatgg	3600
ggccagagat tataagtttg acacaac	3627

<210> 130
 <211> 1029
 <212> PRT
 <213> Homo sapiens
 <400> 130

Met Gly Leu Trp Gly Lys Lys Gly Thr Val Ala Pro His Asp Gln Ser	
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Pro Arg Arg Arg Pro Lys Lys Gly Leu Ile Lys Lys Lys Met Val Lys	
20 25 30	

Arg Glu Lys Gln Lys Arg Asn Met Glu Glu Leu Lys Lys Glu Val Val	
35 40 45	

Met Asp Asp His Lys Leu Thr Leu Glu Glu Leu Ser Thr Lys Tyr Ser	
50 55 60	

Val Asp Leu Thr Lys Gly His Ser His Gln Arg Ala Lys Glu Ile Leu	
65 70 75 80	

Thr Arg Gly Gly Pro Asn Thr Val Thr Pro Pro Pro Thr Thr Pro Glu	
85 90 95	

Trp Val Lys Phe Cys Lys Gln Leu Phe Gly Gly Phe Ser Leu Leu Leu	
100 105 110	

Trp Thr Gly Ala Ile Leu Cys Phe Val Ala Tyr Ser Ile Gln Ile Tyr	
115 120 125	

Phe Asn Glu Glu Pro Thr Lys Asp Asn Leu Tyr Leu Ser Ile Val Leu	
130 135 140	

Ser Val Val Val Ile Val Thr Gly Cys Phe Ser Tyr Tyr Gln Glu Ala	
145 150 155 160	

Lys Ser Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val Pro Gln Gln	
165 170 175	

Ala Leu Val Ile Arg Gly Gly Glu Lys Met Gln Ile Asn Val Gln Glu
180 185 190

Val Val Leu Gly Asp Leu Val Glu Ile Lys Gly Gly Asp Arg Val Pro
195 200 205

Ala Asp Leu Arg Leu Ile Ser Ala Gln Gly Cys Lys Val Asp Asn Ser
210 215 220

Ser Leu Thr Gly Glu Ser Glu Pro Gln Ser Arg Ser Pro Asp Phe Thr
225 230 235 240

His Glu Asn Pro Leu Glu Thr Arg Asn Ile Cys Phe Phe Ser Thr Asn
245 250 255

Cys Val Glu Gly Thr Ala Arg Gly Ile Val Ile Ala Thr Gly Asp Ser
260 265 270

Thr Val Met Gly Arg Ile Ala Ser Leu Thr Ser Gly Leu Ala Val Gly
275 280 285

Gln Thr Pro Ile Ala Ala Glu Ile Glu His Phe Ile His Leu Ile Thr
290 295 300

Val Val Ala Val Phe Leu Gly Val Thr Phe Phe Ala Leu Ser Leu Leu
305 310 315 320

Leu Gly Tyr Gly Trp Leu Glu Ala Ile Ile Phe Leu Ile Gly Ile Ile
325 330 335

Val Ala Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu
340 345 350

Thr Leu Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn
355 360 365

Leu Glu Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp
370 375 380

Lys Thr Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp
385 390 395 400

Phe Asp Met Thr Val Tyr Glu Ala Asp Thr Thr Glu Glu Gln Thr Gly
405 410 415

Lys Thr Phe Thr Lys Ser Ser Asp Thr Trp Phe Met Leu Ala Arg Ile
420 425 430

Ala Gly Leu Cys Asn Arg Ala Asp Phe Lys Ala Asn Gln Glu Ile Leu
435 440 445

Pro Ile Ala Lys Arg Ala Thr Thr Gly Asp Ala Ser Glu Ser Ala Leu
450 455 460

Leu Lys Phe Ile Glu Gln Ser Tyr Ser Ser Val Ala Glu Met Arg Glu
465 470 475 480

Lys Asn Pro Lys Val Ala Glu Ile Pro Phe Asn Ser Thr Asn Lys Tyr
485 490 495

Gln Met Ser Ile His Leu Arg Glu Asp Ser Ser Gln Thr His Val Leu
500 505 510

Met Met Lys Gly Ala Pro Glu Arg Ile Leu Glu Phe Cys Ser Thr Phe
515 520 525

Leu Leu Asn Gly Gln Glu Tyr Ser Met Asn Asp Glu Met Lys Glu Ala
530 535 540

Phe Gln Asn Ala Tyr Leu Glu Leu Gly Gly Leu Gly Glu Arg Val Leu
545 550 555 560

Gly Phe Cys Phe Leu Asn Leu Pro Ser Ser Phe Ser Lys Gly Phe Pro
565 570 575

Phe Asn Thr Asp Glu Ile Asn Phe Pro Met Asp Asn Leu Cys Phe Val
580 585 590

Gly Leu Ile Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro Asp Ala
595 600 605

Val Ser Lys Cys Arg Ser Ala Gly Ile Lys Val Ile Met Val Thr Gly
610 615 620

Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly Val Gly Ile Ile
625 630 635 640

Ser Glu Gly Thr Glu Thr Ala Glu Glu Val Ala Ala Arg Leu Lys Ile
645 650 655

Pro Ile Ser Lys Val Asp Ala Ser Ala Ala Lys Ala Ile Val Val His
660 665 670

Gly Ala Glu Leu Lys Asp Ile Gln Ser Lys Gln Leu Asp Gln Ile Leu
675 680 685

Gln Asn His Pro Glu Ile Val Phe Ala Arg Thr Ser Pro Gln Gln Lys
690 695 700

Leu Ile Ile Val Glu Gly Cys Gln Arg Leu Gly Ala Val Val Ala Val
705 710 715 720

Thr Gly Asp Gly Val Asn Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile
725 730 735

Gly Ile Ala Met Gly Ile Ser Gly Ser Asp Val Ser Lys Gln Ala Ala
740 745 750

Asp Met Ile Leu Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val
755 760 765

Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Met Tyr
770 775 780

Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Met Phe Ile
785 790 795 800

Ile Leu Gly Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile
805 810 815

Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ser
820 825 830

Ala Glu Ser Asp Ile Met Lys Arg Leu Pro Arg Asn Pro Lys Thr Asp
835 840 845

Asn Leu Val Asn His Arg Leu Ile Gly Met Ala Tyr Gly Gln Ile Gly
850 855 860

Met Ile Gln Ala Leu Ala Gly Phe Phe Thr Tyr Phe Val Ile Leu Ala
865 870 875 880

Glu Asn Gly Phe Arg Pro Val Asp Leu Leu Gly Ile Arg Leu His Trp
885 890 895

Glu Asp Lys Tyr Leu Asn Asp Leu Glu Asp Ser Tyr Gly Gln Gln Trp
 900 905 910

Thr Tyr Glu Gln Arg Lys Val Val Glu Phe Thr Cys Gln Thr Ala Phe
 915 920 925

Phe Val Thr Ile Val Val Val Gln Trp Ala Asp Leu Ile Ile Ser Lys
 930 935 940

Thr Arg Arg Asn Ser Leu Phe Gln Gln Gly Met Arg Asn Lys Val Leu
 945 950 955 960

Ile Phe Gly Ile Leu Glu Glu Thr Leu Leu Ala Ala Phe Leu Ser Tyr
 965 970 975

Thr Pro Gly Met Asp Val Ala Leu Arg Met Tyr Pro Leu Lys Ile Thr
 980 985 990

Trp Trp Leu Cys Ala Ile Pro Tyr Ser Ile Leu Ile Phe Val Tyr Asp
 995 1000 1005

Glu Ile Arg Lys Leu Leu Ile Arg Gln His Pro Asp Gly Trp Val
 1010 1015 1020

Glu Arg Glu Thr Tyr Tyr
 1025

<210> 131
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 131
 tgtaatcctg gctgagaatg g

21

<210> 132
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 132
 aagtgagttg cggcgagt

18

<210> 133
 <211> 279
 <212> DNA
 <213> Homo sapiens

 <400> 133
 atgtatgtaa aaattgcaaa acatctcaat gatgtttatg cccccagaa ggtactgtgt 60
 cacgggatct catatattct ggctgtcatt gtcataataa gccactcttg gtcatatgga 120
 aaagcattca gctgctccct gcctttgctc acagcgtgtg gtactctctt agaagctatt 180
 cctgtcctat ttaggcagtt attcctgctt cttgtgttgg acctgaagtc aacagggcca 240
 gcaatagaga agaaagatga tgtgaaggag agcaactga 279

<210> 134
 <211> 92
 <212> PRT
 <213> Homo sapiens

 <400> 134
 Met Tyr Val Lys Ile Ala Lys His Leu Asn Asp Val Tyr Ala Pro Gln
 1 5 10 15

 Lys Val Leu Cys His Gly Ile Ser Tyr Ile Leu Ala Val Ile Val Ile
 20 25 30

 Ile Ser His Ser Trp Ser Tyr Gly Lys Ala Phe Ser Cys Ser Leu Pro
 35 40 45

 Leu Leu Thr Ala Cys Gly Thr Leu Leu Glu Ala Ile Pro Val Leu Phe
 50 55 60

 Arg Gln Leu Phe Leu Leu Leu Val Leu Asp Leu Lys Ser Thr Gly Pro
 65 70 75 80

 Ala Ile Glu Lys Lys Asp Asp Val Lys Glu Ser Asn
 85 90

<210> 135
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 135
 tgctccctgc ctttgctcac

<210> 136
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 136
 ggtacttggt ctcgaacgat gatc 24

<210> 137
 <211> 1569
 <212> DNA
 <213> Homo sapiens

<400> 137
 atgcctgtag ggggtggccc tgagagtgtg ggcaggtgca atggctgtca atgccacata 60
 aagggcaagg ggatctacat cctaaacagt gaaagaccag tgcccggaga ctacatctac 120
 atcaggaaga agaagcagca aaattctgac ccacagccca agaggggtcg gggcagcaga 180
 acctcagcca cagccaatca cagcgggggtc cttcggggag gggcgtggcc tgacaacttc 240
 ggcgacgcgg ctggaccaat ccggacggag gagagcgaag ctctcttgca ctgggcccag 300
 gtgcgctcct cagcgtctcc ggggtggcggg gcgcgcggga tggaggagtc ttgggaggct 360
 gcgcccggag gccaagccgg ggcagagctc ccaatggagc ccgtgggaag cctgggtcccc 420
 acgctggagc agccgcaggt gcccgcgaag gtgcgacaac ctgaagggtcc cgaaagcagc 480
 ccaagtccgg ccggggccgt ggagaaggcg gcgggcgcag gcctggagcc ctcgagcaag 540
 aaaaagccgc cttcgcctcg ccccgggtcc ccgcgcgtgc cgccgctcag cctgggctac 600
 ggggtctgcc ccgagccgcc gtcaccgggc cctgccttgg tcaagctgcc ccggaatggc 660
 gaggcgcccg gggctgagcc tgcgccagc gcctgggcgc ccatggagct gcaggtagat 720
 gtgcgcgtga agcccgtggg cgcggccggt ggcagcagca cgccatcgcc caggccctcc 780
 acgcgcttcc tcaaggtgcc ggtgcccag tcccctgcct tctcccgcca cgcggaacctg 840
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gccagatgcc agcagtcccc cccaggctgg gtgttgccg aggagcactg ttactacttc 1260
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gaaggcacgc tgggtggctgc aaactgcagc actccaagac cctgggtctg tgccaagggg 1560
accagtgga 1569

<210> 138
<211> 522
<212> PRT
<213> Homo sapiens

<400> 138

Met Pro Val Gly Gly Gly Pro Glu Ser Val Gly Arg Cys Asn Gly Cys
1 5 10 15

Gln Cys His Ile Lys Gly Lys Gly Ile Tyr Ile Leu Asn Ser Glu Arg
20 25 30

Pro Val Pro Gly Asp Tyr Ile Tyr Ile Arg Lys Lys Lys Gln Gln Asn
35 40 45

Ser Asp Pro Gln Pro Lys Arg Gly Arg Gly Ser Arg Thr Ser Ala Thr
50 55 60

Ala Asn His Ser Gly Val Leu Arg Gly Gly Ala Trp Pro Asp Asn Phe
65 70 75 80

Gly Asp Ala Ala Gly Pro Ile Arg Thr Glu Glu Ser Glu Ala Pro Leu
85 90 95

His Trp Ala Gln Val Arg Ser Ser Ala Ser Pro Gly Gly Gly Ala Arg
100 105 110

Gly Met Glu Glu Ser Trp Glu Ala Ala Pro Gly Gly Gln Ala Gly Ala
115 120 125

Glu Leu Pro Met Glu Pro Val Gly Ser Leu Val Pro Thr Leu Glu Gln
130 135 140

Pro Gln Val Pro Ala Lys Val Arg Gln Pro Glu Gly Pro Glu Ser Ser
145 150 155 160

Pro Ser Pro Ala Gly Ala Val Glu Lys Ala Ala Gly Ala Gly Leu Glu
165 170 175

Pro Ser Ser Lys Lys Lys Pro Pro Ser Pro Arg Pro Gly Ser Pro Arg
180 185 190

Val Pro Pro Leu Ser Leu Gly Tyr Gly Val Cys Pro Glu Pro Pro Ser
195 200 205

Pro Gly Pro Ala Leu Val Lys Leu Pro Arg Asn Gly Glu Ala Pro Gly
210 215 220

Ala Glu Pro Ala Pro Ser Ala Trp Ala Pro Met Glu Leu Gln Val Asp
225 230 235 240

Val Arg Val Lys Pro Val Gly Ala Ala Gly Gly Ser Ser Thr Pro Ser
245 250 255

Pro Arg Pro Ser Thr Arg Phe Leu Lys Val Pro Val Pro Glu Ser Pro
260 265 270

Ala Phe Ser Arg His Ala Asp Pro Ala His Gln Leu Leu Leu Arg Ala
275 280 285

Pro Ser Gln Gly Gly Thr Trp Gly Arg Arg Ser Pro Leu Ala Ala Ala
290 295 300

Arg Thr Glu Ser Gly Cys Asp Ala Glu Gly Arg Ala Ser Pro Ala Glu
305 310 315 320

Gly Ser Ala Gly Ser Pro Gly Ser Pro Thr Cys Cys Arg Cys Lys Glu
325 330 335

Leu Gly Leu Glu Lys Glu Asp Ala Ala Leu Leu Pro Arg Ala Gly Leu
340 345 350

Asp Gly Asp Glu Lys Leu Pro Arg Ala Val Thr Leu Thr Gly Leu Pro
355 360 365

Met Tyr Val Lys Ser Leu Tyr Trp Ala Leu Ala Phe Met Ala Val Leu
370 375 380

Leu Ala Val Ser Gly Val Val Ile Val Val Leu Ala Ser Arg Ala Gly
385 390 395 400

Ala Arg Cys Gln Gln Cys Pro Pro Gly Trp Val Leu Ser Glu Glu His
405 410 415

Cys Tyr Tyr Phe Ser Ala Glu Ala Gln Ala Trp Glu Ala Ser Gln Ala
420 425 430

Phe Cys Ser Ala Tyr His Ala Thr Leu Pro Leu Leu Ser His Thr Gln
435 440 445

Asp Phe Leu Gly Arg Tyr Pro Val Ser Arg His Ser Trp Val Gly Ala
450 455 460

Trp Arg Gly Pro Gln Gly Trp His Trp Ile Asp Glu Ala Pro Leu Pro
465 470 475 480

Pro Gln Leu Leu Pro Glu Asp Gly Glu Asp Asn Leu Asp Ile Asn Cys
485 490 495

Gly Ala Leu Glu Glu Gly Thr Leu Val Ala Ala Asn Cys Ser Thr Pro
500 505 510

Arg Pro Trp Val Cys Ala Lys Gly Thr Gln
515 520

<210> 139
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 139
gagaaggagg atgcggcg

18

<210> 140
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 140
ggaccacaat gacaacccca g

21

<210> 141
<211> 2217

<212> DNA
<213> Homo sapiens

<400> 141

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ctgaagaaat	tattgccacg	tgttcccaaa	aacagtgtcc	tgagtgatga	aatgacaaaag	180
cttcacaaaag	gagctaagcc	atgcaaatca	aatacatttg	gatgttttcc	tattcatcag	240
gctgtacttt	caggttccaa	agaatgcatg	gaaataatat	tgaagtgttg	tgaagagcac	300
gggtacagca	gacagtgtca	catcaacttt	gtggataacg	ggaaagccag	ccctctccat	360
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tgtactcctc	tacattatgc	atgtagacag	gggggccctg	gttctgtaaa	taacctactt	540
ggctttaatg	tgtccattca	ttccaaaagc	aaagataaga	aatcacctct	gcattttgca	600
gccagttatg	ggcgtatcaa	tacctgtcag	aggctcctac	aagacataag	tgatacgagg	660
cttctgaatg	aaggggacct	tcatggaatg	actcctctcc	atctggcagc	aaagaatgga	720
catgataaag	tagttcagct	tcttctgaaa	aaaggtgcat	tgtttctcag	atgggatgaa	780
tgtcttaagg	tttttagtca	ttattctcca	aacaataaat	gtccaatttt	ggaaatgatc	840
gaatacctcc	ctgaatgcat	gaagaaagtt	ctacccttct	tttctaattg	tcacgtaaga	900
cctgctccaa	accagaatca	aataaaccat	ggagaacaca	ggttggctta	cggattttata	960
gcccataatga	taaatctagg	atcttactgt	cttgggtctca	taccaatgac	ctttcttggt	1020
gtcagaataa	aaccaggaat	ggctttcaac	tctgctggaa	tcatcaataa	aactagtgat	1080
cattcagaaa	tactagataa	catgaattca	agtctaataa	caatttgat	gatttttagtt	1140
ttttgctcaa	gtatattagg	gtatgtcaaa	gaagtgggtc	aaattttcca	acagaaaagg	1200
aattacttta	tggatattag	cagtagtact	gaatggatta	tcaacacgat	gggccccatt	1260
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gaaccatttc	tgaagaataa	attggcacat	ccagttctgt	cctttgcaca	gcttattttcc	1500
ttcacagtat	ttgcccgaat	tgtcctcatg	aatttactta	ttggtttggc	agttggtgac	1560
attgctgagg	tccagaaaca	tgcatcattg	aagaggatag	ctatgcagaa	gctgccatgc	1620
tgttgcatac	gcaaagtgga	tgggaaatcc	accgccgtat	gtcccaacaa	accagatgt	1680

gatgggacat tatttcaagt cctactcgct ctagggcccc taccctaga agaaaataga 1740
aacataaaaa gttttcttcc tactgagatc actgttaaga ggactcacga acaccttcct 1800
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cttctctga atgtagtaca ctctcttgc tctgccttca gagggttg ccagatcttt 1920
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tgcacagtga aggtggtcca gagagatgac atctctgtgt ggagtgtgga tttcagggtg 2100
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<210> 142
<211> 738
<212> PRT
<213> Homo sapiens

<400> 142

Met Val Cys Thr Phe Asp Ser Glu Leu Leu Asn Cys Gln Arg Lys Asp
1 5 10 15

Glu Tyr Asn Gln Phe Gln Thr Tyr Arg Ala His Lys Ile Lys Ala Lys
20 25 30

Arg Ser Ile Ala Thr Pro Glu Asn Leu Lys Lys Leu Leu Pro Arg Val
35 40 45

Pro Lys Asn Ser Ala Leu Ser Asp Glu Met Thr Lys Leu His Lys Gly
50 55 60

Ala Lys Pro Cys Lys Ser Asn Thr Phe Gly Cys Phe Pro Ile His Gln
65 70 75 80

Ala Val Leu Ser Gly Ser Lys Glu Cys Met Glu Ile Ile Leu Lys Phe
85 90 95

Gly Glu Glu His Gly Tyr Ser Arg Gln Cys His Ile Asn Phe Val Asp
100 105 110

Asn Gly Lys Ala Ser Pro Leu His Leu Ala Val Gln Asn Gly Asp Leu
115 120 125

Glu Met Met Lys Met Cys Leu Asp Asn Gly Val Gln Ile Asp Leu Val
130 135 140

Glu Met Gln Gln Ile Lys Glu Leu Val Met Asp Glu Asp Asn Asp Gly
 145 150 155 160

Cys Thr Pro Leu His Tyr Ala Cys Arg Gln Gly Gly Pro Gly Ser Val
 165 170 175

Asn Asn Leu Leu Gly Phe Asn Val Ser Ile His Ser Lys Ser Lys Asp
 180 185 190

Lys Lys Ser Pro Leu His Phe Ala Ala Ser Tyr Gly Arg Ile Asn Thr
 195 200 205

Cys Gln Arg Leu Leu Gln Asp Ile Ser Asp Thr Arg Leu Leu Asn Glu
 210 215 220

Gly Asp Leu His Gly Met Thr Pro Leu His Leu Ala Ala Lys Asn Gly
 225 230 235 240

His Asp Lys Val Val Gln Leu Leu Leu Lys Lys Gly Ala Leu Phe Leu
 245 250 255

Arg Trp Asp Glu Cys Leu Lys Val Phe Ser His Tyr Ser Pro Asn Asn
 260 265 270

Lys Cys Pro Ile Leu Glu Met Ile Glu Tyr Leu Pro Glu Cys Met Lys
 275 280 285

Lys Val Leu Pro Phe Phe Ser Asn Val His Val Arg Pro Ala Pro Asn
 290 295 300

Gln Asn Gln Ile Asn His Gly Glu His Arg Leu Ala Tyr Gly Phe Ile
 305 310 315 320

Ala His Met Ile Asn Leu Gly Phe Tyr Cys Leu Gly Leu Ile Pro Met
 325 330 335

Thr Phe Leu Val Val Arg Ile Lys Pro Gly Met Ala Phe Asn Ser Ala
 340 345 350

Gly Ile Ile Asn Lys Thr Ser Asp His Ser Glu Ile Leu Asp Asn Met
 355 360 365

Asn Ser Ser Leu Ile Thr Ile Cys Met Ile Leu Val Phe Cys Ser Ser
 370 375 380

Ile Leu Gly Tyr Val Lys Glu Val Val Gln Ile Phe Gln Gln Lys Arg
 385 390 395 400

Asn Tyr Phe Met Asp Ile Ser Ser Ser Thr Glu Trp Ile Ile Asn Thr
 405 410 415

Met Gly Pro Ile Leu Val Leu Pro Leu Phe Thr Glu Ile Ala Ala His
 420 425 430

Leu Gln Phe Glu Asn Cys Gly Ile Phe Ile Val Ile Leu Glu Val Ile
 435 440 445

Phe Lys Thr Leu Leu Arg Ser Ala Val Val Phe Phe Phe Leu Leu Leu
 450 455 460

Ala Phe Gly Leu Ser Phe Tyr Val Leu Leu Asn Leu Gln Ser Phe Leu
 465 470 475 480

Glu Pro Phe Leu Lys Asn Lys Leu Ala His Pro Val Leu Ser Phe Ala
 485 490 495

Gln Leu Ile Ser Phe Thr Val Phe Ala Pro Ile Val Leu Met Asn Leu
 500 505 510

Leu Ile Gly Leu Ala Val Gly Asp Ile Ala Glu Val Gln Lys His Ala
 515 520 525

Ser Leu Lys Arg Ile Ala Met Gln Lys Leu Pro Cys Cys Cys Ile Arg
 530 535 540

Lys Val Asp Arg Lys Ser Thr Ala Val Cys Pro Asn Lys Pro Arg Cys
 545 550 555 560

Asp Gly Thr Leu Phe Gln Val Leu Leu Ala Leu Gly Pro Leu Pro Leu
 565 570 575

Glu Glu Asn Arg Asn Ile Lys Ser Phe Leu Pro Thr Glu Ile Thr Val
 580 585 590

Lys Arg Thr His Glu His Leu Pro Ser Ala Gly Phe Gly His His Gly
 595 600 605

Lys His Thr Leu Ser Leu Leu Leu Val Glu Glu Trp Leu Pro Leu Asn
 610 615 620

Val Val His Ser Ser Cys Ser Ala Phe Arg Val Val Gly Gln Ile Phe
 625 630 635 640

Pro Ile Arg His Phe Gln Trp Ile His Val Asn Glu Pro His Thr Gly
 645 650 655

Asn Leu Lys Glu Lys Leu Ala Ala Pro Tyr Ile Thr His Gln Ile Lys
 660 665 670

Pro Phe Leu Arg Ala Ala Gly Phe Cys Thr Val Lys Val Val Gln Arg
 675 680 685

Asp Asp Ile Ser Val Trp Ser Val Asp Phe Arg Trp Leu Asn Ala Trp
 690 695 700

Glu Ala Ala Ile Arg Lys Gln Ser Leu Arg Gln Ser Glu Met Glu Glu
 705 710 715 720

Leu Ser Cys Ser Leu Leu Leu Arg Val Thr Asp Val His Thr Arg Ser
 725 730 735

Leu Tyr

<210> 143
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 143
 ttccttactc tccgctttcc

20

<210> 144
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 144
 aactttgtgg ataacgggaa

20

<210> 145
 <211> 1155

<212> DNA
 <213> Homo sapiens

<400> 145
 atgcagtcctc tcctctcgcc ggtgaccaag gcgatcctgg tggccctctt catcttcgcc 60
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 cgtgcggggcg ctttgggggg ccacgggttg ggagcccca cttcggggag gacgcggaat 180
 ccggacgcgg gactgaacct gaggattcac ggagcccggt gctcccctat ggggcacggg 240
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 aaggcgcata ggcgctcccg cctgtggccg ccaccgggtg agcagaacgc gggctctcgg 360
 gtgggtccaa tgcgctatgg cacaccaggc gctatcgggt ccctagccct ctgctccggc 420
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 gtcccagaaa tttctagaag caaatctcgc attcgtgacc gccagacctt cgggatgtac 600
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 <213> Homo sapiens

<400> 146
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Pro Gly Arg Ala Gly Glu Cys Ala Arg Ala Gly Ala Leu Gly Gly His
 35 40 45
 Gly Trp Gly Ala Pro Thr Ser Gly Arg Thr Arg Asn Pro Asp Ala Gly
 50 55 60
 Leu Asn Pro Arg Ile His Gly Ala Arg Gly Ser Pro Met Gly His Gly
 65 70 75 80
 Lys Arg Gln Met Arg Val Gln Arg Gly Pro Ser His Pro Pro Pro Gly
 85 90 95
 Arg Leu Gly Ser Lys Ala His Arg Arg Ser Arg Leu Trp Pro Pro Pro
 100 105 110
 Val Gln Gln Asn Ala Gly Ser Arg Val Gly Pro Met Arg Tyr Gly Thr
 115 120 125
 Pro Gly Ala Ile Gly Ser Leu Ala Leu Cys Ser Gly Gly Gly Asp Pro
 130 135 140
 Ala Leu Lys Phe Pro Ile Thr Ser Met Asp Lys His Gly Lys Ile Met
 145 150 155 160
 Ser Trp Lys Asn Ser Ile Ala Leu Gln Ile Gln Thr Arg His Phe Ala
 165 170 175
 His Glu Thr Arg Val Pro Glu Ile Ser Arg Ser Lys Ser Arg Ile Arg
 180 185 190
 Asp Arg Gln Thr Tyr Gly Met Tyr His Phe Gly Asn Phe Gly Glu Glu
 195 200 205
 Arg Ile Lys Ala Glu Met Arg Ile Gln Lys Ala Cys His Leu Lys Ile
 210 215 220
 Lys Lys Ser Ser Leu Asp Ala Asn Gly Lys Val Asp Asp Gly Glu Asp
 225 230 235 240
 Asp Asp Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly Asp Asp Asp
 245 250 255
 Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly
 260 265 270

Glu Asp Asp Gly Glu Asp Asp Asp Gly Asp Asp Asp Gly Glu Asp Asp
 275 280 285

Asp Gly Asp Asp Asp Gly Asp Asp Asp Gly Glu Asp Asp Asp Gly Glu
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Asp Asp Asp Gly Asp Ser Glu Asp Asp Gly Glu Asp Gly Asp Asp Asp
 305 310 315 320

Gly Glu Asp Asp Asp Gly Asp Ser Glu Asp Asp Gly Asp Asp Gly Asp
 325 330 335

Asp Asp Gly Glu Asp Asp Asp His Gly Asp Asp Val Arg Met Met Met
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<400> 148
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 <212> DNA
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tcta 4384

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<212> PRT
<213> Homo sapiens

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<400> 150

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Leu Cys Gly Gln Pro Ala Asp Tyr Leu Val Glu Glu Lys His Phe Thr
20          25          30

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Thr Leu Val Cys Phe Ile Val Val Leu Gly Gly Leu Leu Lys Met Cys
35          40          45

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Leu Lys Asn Cys Glu Val Ile Val Leu Thr Ile Leu Ser Leu Ser Gly
50          55          60

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Phe Val Ile Gly His Met Ala Tyr Asn Ser Val Glu Val His Gln Ile
65          70          75          80

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Val Tyr Pro Leu Leu Arg Thr Ser Ser Phe Ser Leu Tyr Ser Tyr Phe
85          90          95

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Ser Pro Leu Ile Ile Phe Met Val Ala Leu Asp Val Glu Phe Tyr Thr
100          105          110

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Leu Lys Lys Met Phe Trp Gln Val Leu Leu Thr Gly Leu Ile Ser Phe
115 120 125

Ser Thr Ala Ser Ile Ile Ile Gly Tyr Val Val Ile Lys Phe Asn Lys
130 135 140

Asp Ser Trp Asp Leu Gln Ser Cys Leu Leu Phe Ser Ile Thr Leu Gly
145 150 155 160

Ile Ile Asp Pro Leu Arg Ser Val Asn Ser Leu Lys Thr Ile Gly Ile
165 170 175

Ser Lys Ile Tyr Ile Asp Leu Ile Arg Gly Glu Ser Leu Ile Ile Cys
180 185 190

Ser Ile Ala Ser Ile Phe Phe Gly Asn Phe Arg Gly Asn Arg Ile His
195 200 205

Phe Ser Ile Phe Arg Asp Leu His Val Gly Ile Glu Leu Ser Tyr Asp
210 215 220

Ile Leu Gly Ser Ile Ile Phe Gly Tyr Trp Cys Ala Lys Ile Ile Gln
225 230 235 240

Cys Ile Leu Ala Asp Val Phe Ser Asn Met Leu Thr Asn Ile Ile Leu
245 250 255

Cys Phe Ser Met Val Tyr Met Thr Phe Tyr Ile Val Glu Phe Leu Gly
260 265 270

Met Ser Gly Thr Leu Ala Leu Ala Ala Val Gly Leu Asn Leu Asp Ser
275 280 285

Leu Thr Phe Lys Pro Lys Ile Glu Leu Val Ile Thr Lys Phe Leu Arg
290 295 300

Ile Phe Ser Ser Val Tyr Glu His Leu Ile Tyr Ala Phe Phe Gly Ile
305 310 315 320

Val Ile Gly Cys Gly Glu Leu Ser His Tyr Glu Phe His Thr Ile Pro
325 330 335

Phe Ile Phe Ile Leu Phe Thr Thr Val Asn Leu Val Arg Leu Leu Thr
340 345 350

Ile Leu Leu Val Ser Pro Ile Leu Met His Ser Asn Tyr Glu Tyr Asn
 355 360 365

Trp Arg Trp Gly Val Val Ile Thr Trp Ser Gly Ile Lys Gly Val Phe
 370 375 380

Asn Leu Leu Trp Ala Pro Asp Val Tyr Asn Leu Ala Glu Arg Lys Val
 385 390 395 400

Glu Val Pro Gln Met Phe Ile Leu Tyr Val Gln Val Ile Ser Leu Leu
 405 410 415

Thr Met Gly Ile Asn Ser Tyr Val Met Thr Gln Ser Ala Arg Lys Leu
 420 425 430

Asp Leu Cys Val Leu Ser Leu Pro Arg Gln Met Ile Leu Gln Asn Ala
 435 440 445

Thr Gln His Ile Gln Glu Ile Val Gln Asn Thr Ile Thr Leu Phe Lys
 450 455 460

Thr Glu Lys Ile Leu Thr Asn Val Asn Trp Thr Leu Val Glu Asp Lys
 465 470 475 480

Thr Arg Ile Glu Tyr Ile Pro Phe Ser His Val Ser His Asn Asp Met
 485 490 495

Lys Thr Glu Ser Thr Thr Asp Glu Ala Leu Met Glu Glu Ala Arg Leu
 500 505 510

His Val Ala Ala Ile Gln Met Ser Ser Phe Glu Lys Gln Arg Asn Asn
 515 520 525

Gly Ile Leu Glu Ile Glu Ala Ala Arg Ile Leu Ile Gly Ala Ala Lys
 530 535 540

Cys Tyr Tyr Ser Ile Gln Gly Lys Phe Met Ser Ile Tyr Asp Val Ser
 545 550 555 560

Thr Tyr Met Arg Thr Arg Ser Trp Leu Ile Lys Phe Lys Asn Val Leu
 565 570 575

Thr Phe Leu Glu Tyr Cys Ile Glu Lys Ile His Phe Ile Pro Pro Glu
 580 585 590

Ser Asn Thr Phe Leu Thr Phe Ile Phe His Ile Val Phe Ser Glu Glu
595 600 605

Phe Glu Tyr Thr Gly Gln Ile Ile Asn Leu Ile Tyr Ile Tyr Pro Met
610 615 620

Ile Ile His Leu Trp Pro Met Ala Arg Gly Leu Asn Val Ser Ala Leu
625 630 635 640

Ile Ser Ile Asn Tyr Tyr Phe Met Phe Leu Tyr Val Leu Glu Ser Thr
645 650 655

Leu Lys Ile Ile Ile Leu Lys Arg Lys Tyr Phe Gln Gln Cys Trp Asn
660 665 670

Thr Leu Glu Phe Phe Ile Leu Val Ile Gly Ile Ile Asp Ile Phe Cys
675 680 685

Val Tyr Phe Val Lys Leu Arg Pro Asp Asn Leu Ala Leu Ile Gln Leu
690 695 700

Thr Val Ile Met Gly Tyr Leu Arg Ile Ile Arg Phe Leu Pro Leu Phe
705 710 715 720

Lys Ile Ile Val Pro Ile Leu Ile Arg Ile Ala Asp Val Gln Ile Lys
725 730 735

Lys Arg Leu Ser Leu Met Tyr Ser Ile Thr Lys Gly Tyr Ile Lys Ser
740 745 750

Gln Glu Asp Ala Lys Leu Leu Ile Lys Gln Ile Ala Val Cys Glu Ser
755 760 765

Ile Tyr Gln Lys Leu Cys Glu Ile Leu Glu Thr Asn Lys Gln Asp Ala
770 775 780

Val Lys Glu Leu Val Leu Met Glu His Glu Gly Arg Asp Val Val Ile
785 790 795 800

Ala Leu Lys Thr Lys Gln Ala Ile Arg Asn Val Ile Ala Lys Ala Leu
805 810 815

Lys Asn Leu Thr Phe Leu Cys Ser Arg Gly Ile Ile Asp Lys His Glu
820 825 830

Val Ile Glu Ile Asn Lys Val Leu Leu Lys Lys Leu Lys Ala Leu Asn
835 840 845

Asn Phe Pro Lys Ala Ile Pro Pro Pro Thr Pro Asp Ile Tyr Leu His
850 855 860

Asn Ile Ile Trp Leu Glu Gly Lys Asp Val Leu Ile Asp Phe Phe Lys
865 870 875 880

Glu Arg Ala Lys Leu Ala Cys Phe Asp Ser Gly Asp Thr Ile Cys Lys
885 890 895

Gly Gly Glu Met Pro Gln Gly Ile Tyr Leu Ile Ile Ser Gly Met Ala
900 905 910

Ile Leu His Ser Leu Ser Pro Thr Phe Gly Ile Glu Ser Asn Gln Arg
915 920 925

Cys Asp Arg Gly Ser Arg Asp Met Phe Thr Glu Phe Cys Thr Thr Gly
930 935 940

Asp Ile Ile Gly Glu Leu Ser Cys Leu Leu Lys Arg Glu Ile Glu Tyr
945 950 955 960

Thr Val Ile Cys Glu Thr Ser Leu Gln Ala Cys Phe Ile Ser Leu Glu
965 970 975

Asp Leu Tyr Glu Gly Phe Asp Ala Phe Trp Pro Ser Leu Glu Tyr Lys
980 985 990

Ile Trp Leu Lys Leu Ala Leu Ser Thr Ala Tyr Gln Tyr Phe Glu Ser
995 1000 1005

Ser Leu Ile Asp Glu Asp Leu Arg Phe Gln Asn Cys Val Met Phe
1010 1015 1020

Asn Gln Ala Tyr Val Glu Thr Leu Ser Ser Tyr Ser Asp Met Ile
1025 1030 1035

Ile Asp Asn Met Thr Met Lys Phe Val Ile Ile Val Tyr Gly Ser
1040 1045 1050

Val Ile Asp Thr Lys Thr Glu Glu Pro Tyr Phe Ala Pro Cys Ile
1055 1060 1065

Ile Pro Thr Thr Cys Glu Gln Val Gln Gly Thr Ser Asp Leu Ser
 1070 1075 1080

Lys Leu Leu Ile Ile Gln Ala Ser Glu Leu Thr Gln Arg Asn Ser
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Asn Thr Asn Val Met Ala Ser Val Asn Thr Val Phe Glu Gln Pro
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Gly Lys Asn Ile Asn Gly Arg Gln Lys Met Ser
 1115 1120

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<400> 152
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Glu Phe Pro Ser Pro Cys Leu Asp Ser Lys Thr Lys Val Val Met Lys
 35 40 45

Gly Gln Asn Val Ser Met Phe Cys Ser His Lys Asn Lys Ser Leu Gln
 50 55 60

Ile Thr Tyr Ser Leu Phe Arg Arg Lys Thr His Leu Gly Thr Gln Asp
 65 70 75 80

Gly Lys Gly Glu Pro Ala Ile Phe Asn Leu Ser Ile Thr Glu Ala His
 85 90 95

Glu Ser Gly Pro Tyr Lys Cys Lys Ala Gln Val Thr Ser Cys Ser Lys
 100 105 110

Tyr Ser Arg Asp Phe Ser Phe Thr Ile Val Asp Pro Val Thr Ser Pro
 115 120 125

Val Leu Asn Ile Met Val Ile Gln Thr Glu Thr Asp Arg His Ile Thr
 130 135 140

Leu His Cys Leu Ser Val Asn Gly Ser Leu Pro Ile Asn Tyr Thr Phe
 145 150 155 160

Phe Glu Asn His Val Ala Ile Ser Pro Ala Ile Ser Lys Tyr Asp Arg
 165 170 175

Glu Pro Ala Glu Phe Asn Leu Thr Lys Lys Asn Pro Gly Glu Glu Glu
 180 185 190

Glu Tyr Arg Cys Glu Ala Lys Asn Arg Leu Pro Asn Tyr Ala Thr Tyr
 195 200 205

Ser His Pro Val Thr Met Pro Ser Thr Gly Gly Asp Ser Cys Pro Phe
 210 215 220

Cys Leu Lys Leu Leu Leu Pro Gly Leu Leu Leu Leu Leu Val Val Ile
 225 230 235 240

Ile Leu Ile Leu Ala Phe Trp Val Leu Pro Lys Tyr Lys Thr Arg Lys
 245 250 255

Ala Met Arg Asn Asn Val Pro Arg Asp Arg Gly Asp Thr Ala Met Glu
 260 265 270

Val Gly Ile Tyr Ala Asn Ile Leu Glu Lys Gln Ala Lys Glu Glu Ser
 275 280 285

Val Pro Glu Val Gly Ser Arg Pro Cys Val Ser Thr Ala Gln Asp Glu
 290 295 300

Ala Lys His Ser Gln Glu Leu Gln Tyr Ala Thr Pro Val Phe Gln Glu
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Val Tyr Ser Glu Ser
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<220>
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<400> 156
acagagtgag actccatcct g 21

<210> 157
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<213> Homo sapiens

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 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 158

Met Cys Arg Cys Pro Pro Glu His His Asp Gly Arg Met Thr Ser Ala
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Glu Val Gly Ala Ala Ala Gly Gly Ala Gln Ala Ala Gly Pro Pro Glu
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Trp Pro Pro Gly Ser Pro Gln Ala Leu Arg Gln Pro Gly Arg Ala Arg
 35 40 45

Val Ala Met Ala Ala Leu Val Trp Leu Leu Ala Gly Ala Ser Met Ser
 50 55 60

Ser Leu Asn Lys Trp Ile Phe Thr Val His Gly Phe Gly Arg Pro Leu
 65 70 75 80

Leu Leu Ser Ala Leu His Met Leu Val Ala Ala Leu Ala Cys His Arg
 85 90 95

Gly Ala Arg Arg Pro Met Pro Gly Gly Thr Arg Cys Arg Val Leu Leu
 100 105 110

Leu Ser Leu Thr Phe Gly Thr Ser Met Ala Cys Gly Asn Val Gly Leu
 115 120 125

Arg Ala Val Pro Leu Asp Leu Ala Gln Leu Val Thr Thr Thr Thr Pro
 130 135 140

Leu Phe Thr Leu Ala Leu Ser Ala Leu Leu Leu Gly Arg Arg His His
 145 150 155 160

Pro Leu Gln Leu Ala Ala Met Gly Pro Leu Cys Leu Gly Ala Ala Cys
 165 170 175

Ser Leu Ala Gly Glu Phe Arg Thr Pro Pro Thr Gly Cys Gly Phe Leu
 180 185 190

Leu Ala Ala Thr Cys Leu Arg Gly Leu Lys Ser Val Gln Gln Ser Ala
 195 200 205

Leu Leu Gln Glu Glu Arg Leu Asp Ala Val Thr Leu Leu Tyr Ala Thr
 210 215 220

Ser Leu Pro Ser Phe Cys Leu Leu Ala Gly Ala Ala Leu Val Leu Glu
 225 230 235 240

Ala Gly Val Ala Pro Pro Pro Thr Ala Gly Asp Ser Arg Leu Trp Ala
 245 250 255

Cys Ile Leu Leu Ser Cys Leu Leu Ser Val Leu Tyr Asn Leu Ala Ser
 260 265 270

Phe Ser Leu Leu Ala Leu Thr Ser Ala Leu Thr Val His Val Leu Gly
 275 280 285

Asn Leu Thr Val Val Gly Asn Leu Ile Leu Ser Arg Leu Leu Phe Gly
 290 295 300

Ser Arg Leu Ser Ala Leu Ser Tyr Val Gly Ile Ala Leu Thr Leu Ser
 305 310 315 320

Gly Met Phe Leu Tyr His Asn Cys Glu Phe Val Ala Ser Trp Ala Ala
 325 330 335

Arg Arg Gly Leu Trp Arg Arg Asp Gln Pro Ser Lys Gly Leu
 340 345 350

<210> 159
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 159
 caagtcggtt cagcaaagtg c

21

<210> 160
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 <212> DNA
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<220>

<223> Oligonucleotide

<400> 160

cctgaaagag tgagtgcgat g

21

<210> 161

<211> 963

<212> DNA

<213> Homo sapiens

<400> 161

gactacacaa ggactgaacc agaaggaaga ggacagagca aagccatgaa catcatccta 60

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ttcattcctc agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 180

catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat attggttctg 240

tgggatatta ataagcgcgg tgtggaggaa actgcagctg agtgccgaaa actaggcgtc 300

actgcgcatg cgtatgtggt agactgcagc aacagagaag agatctatcg ctctctaaat 360

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ccagccgatac ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 480

ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag aaatcatggc 540

cacatcgta cagtggcttc agtgtgcggc cacgaaggga ttccttacct catcccatat 600

tgttccagca aatttgccgc tgttggcttt cacagaggtc tgacatcaga acttcaggcc 660

ttgggaaaaa ctggtatcaa aacctcatgt ctctgcccag tttttgtgaa tactgggttc 720

acaaaaaatc caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 780

ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta tatcaatatc 840

tttctgagac tacagaatcc tgataatatt aaaaacattg gtttggcact agcagcagtc 900

aaacgaacaa gattaattac ctgtcttctt gtttctcaag aatatttacg tagtttttca 960

tag 963

<210> 162

<211> 305

<212> PRT

<213> Homo sapiens

<400> 162

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Ile Thr Ile Ile Tyr
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Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
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Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
 35 40 45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val
 50 55 60

Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys
 65 70 75 80

Arg Lys Leu Gly Val Thr Ala His Ala Tyr Val Val Asp Cys Ser Asn
 85 90 95

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly
 100 105 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp
 115 120 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn
 130 135 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met
 145 150 155 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His
 165 170 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala
 180 185 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys
 195 200 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly
 210 215 220

Phe Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp
 225 230 235 240

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met
 245 250 255

Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Asn Pro
 260 265 270

Asp Asn Ile Lys Asn Ile Gly Leu Ala Leu Ala Ala Val Lys Arg Thr
 275 280 285

Arg Leu Ile Thr Cys Leu Pro Val Ser Gln Glu Tyr Leu Arg Ser Phe
 290 295 300

Ser
 305

<210> 163
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 163
 ggtctgacat cagaacttca g 21

<210> 164
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 164
 tgcatacatc tctggctgga g 21

<210> 165
 <211> 6014
 <212> DNA
 <213> Homo sapiens

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caatattttt	gcacatatata	agggttgggg	aggaaagaga	cacaaacgta	tttaacacag	5880

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<210> 166
 <211> 817
 <212> PRT
 <213> Homo sapiens

<400> 166

Met Lys Gln Cys Val Arg Leu Thr Val His Pro Asn Asn Ile Ser Val
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Ser Gln Tyr Asn Val Leu Leu Val Leu Glu Thr Tyr Asn Val Pro Glu
 20 25 30

Leu Ser Ala Gly Val Asn Cys Thr Phe Glu Asp Leu Ser Glu Met Asp
 35 40 45

Gly Leu Val Val Gly Asn Gln Ile Gln Cys Tyr Ser Pro Ala Ala Lys
 50 55 60

Glu Val Pro Arg Ile Ile Thr Glu Asn Gly Asp His His Val Val Gln
 65 70 75 80

Leu Gln Leu Lys Ser Lys Glu Thr Gly Met Thr Phe Ala Ser Thr Ser
 85 90 95

Phe Val Phe Tyr Asn Cys Ser Val His Asn Ser Cys Leu Ser Cys Val
 100 105 110

Glu Ser Pro Tyr Arg Cys His Trp Cys Lys Tyr Arg His Val Cys Thr
 115 120 125

His Asp Pro Lys Thr Cys Ser Phe Gln Glu Gly Arg Val Lys Leu Pro
 130 135 140

Glu Asp Cys Pro Gln Leu Leu Arg Val Asp Lys Ile Leu Val Pro Val
 145 150 155 160

Glu Val Ile Lys Pro Ile Thr Leu Lys Ala Lys Asn Leu Pro Gln Pro
 165 170 175

Gln Ser Gly Gln Arg Gly Tyr Glu Cys Ile Leu Asn Ile Gln Gly Ser
 180 185 190

Glu Gln Arg Val Pro Ala Leu Arg Phe Asn Ser Ser Ser Val Gln Cys
195 200 205

Gln Asn Thr Ser Tyr Ser Tyr Glu Gly Met Glu Ile Asn Asn Leu Pro
210 215 220

Val Glu Leu Thr Val Val Trp Asn Gly His Phe Asn Ile Asp Asn Pro
225 230 235 240

Ala Gln Asn Lys Val His Leu Tyr Lys Cys Gly Ala Met Arg Glu Ser
245 250 255

Cys Gly Leu Cys Leu Lys Ala Asp Pro Asp Phe Ala Cys Gly Trp Cys
260 265 270

Gln Gly Pro Gly Gln Cys Thr Leu Arg Gln His Cys Pro Ala Gln Glu
275 280 285

Ser Gln Trp Leu Glu Leu Ser Gly Ala Lys Ser Lys Cys Thr Asn Pro
290 295 300

Arg Ile Thr Glu Ile Ile Pro Val Thr Gly Pro Arg Glu Gly Gly Thr
305 310 315 320

Lys Val Thr Ile Arg Gly Glu Asn Leu Gly Leu Glu Phe Arg Asp Ile
325 330 335

Ala Ser His Val Lys Val Ala Gly Val Glu Cys Ser Pro Leu Val Asp
340 345 350

Gly Tyr Ile Pro Ala Glu Gln Ile Val Cys Glu Met Gly Glu Ala Lys
355 360 365

Pro Ser Gln His Ala Gly Phe Val Glu Ile Cys Val Ala Val Cys Arg
370 375 380

Pro Glu Phe Met Ala Arg Ser Ser Gln Leu Tyr Tyr Phe Met Thr Leu
385 390 395 400

Thr Leu Ser Asp Leu Lys Pro Ser Arg Gly Pro Met Ser Gly Gly Thr
405 410 415

Gln Val Thr Ile Thr Gly Thr Asn Leu Asn Ala Gly Ser Asn Val Val
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Val Met Phe Gly Lys Gln Pro Cys Leu Phe His Arg Arg Ser Pro Ser
 435 440 445

Tyr Ile Val Cys Asn Thr Thr Ser Ser Asp Glu Val Leu Glu Met Lys
 450 455 460

Val Ser Val Gln Val Asp Arg Ala Lys Ile His Gln Asp Leu Val Phe
 465 470 475 480

Gln Tyr Val Glu Asp Pro Thr Ile Val Arg Ile Glu Pro Glu Trp Ser
 485 490 495

Ile Val Ser Gly Asn Thr Pro Ile Ala Val Trp Gly Thr His Leu Asp
 500 505 510

Leu Ile Gln Asn Pro Gln Ile Arg Ala Lys His Gly Gly Lys Glu His
 515 520 525

Ile Asn Ile Cys Glu Val Leu Asn Ala Thr Glu Met Thr Cys Gln Ala
 530 535 540

Pro Ala Leu Ala Leu Gly Pro Asp His Gln Ser Asp Leu Thr Glu Arg
 545 550 555 560

Pro Glu Glu Phe Gly Phe Ile Leu Asp Asn Val Gln Ser Leu Leu Ile
 565 570 575

Leu Asn Lys Thr Asn Phe Thr Tyr Tyr Pro Asn Pro Val Phe Glu Ala
 580 585 590

Phe Gly Pro Ser Gly Ile Leu Glu Leu Lys Pro Gly Thr Pro Ile Ile
 595 600 605

Leu Lys Gly Lys Asn Leu Ile Pro Pro Val Ala Gly Gly Asn Val Lys
 610 615 620

Leu Asn Tyr Thr Val Leu Val Gly Glu Lys Pro Cys Thr Val Thr Val
 625 630 635 640

Ser Asp Val Gln Leu Leu Cys Glu Ser Pro Asn Leu Ile Gly Arg His
 645 650 655

Lys Val Met Ala Arg Val Gly Gly Met Glu Tyr Ser Pro Gly Met Val
 660 665 670

Tyr Ile Ala Pro Asp Ser Pro Leu Ser Leu Pro Ala Ile Val Ser Ile
675 680 685

Ala Val Ala Gly Gly Leu Leu Ile Ile Phe Ile Val Ala Val Leu Ile
690 695 700

Ala Tyr Lys Arg Lys Ser Arg Glu Ser Asp Leu Thr Leu Lys Arg Leu
705 710 715 720

Gln Met Gln Met Asp Asn Leu Glu Ser Arg Val Ala Leu Glu Cys Lys
725 730 735

Glu Gly Thr Glu Trp Pro His Ala Gly Gly His Val Cys Val Arg Val
740 745 750

Cys Ile Cys Val Cys Met His Ile Cys Val Cys Val Cys Ile Cys Phe
755 760 765

Ile Tyr Lys Gln Ala Gly Trp Ala Ala Val Gly Ser Ala Gly Gly Trp
770 775 780

Arg Cys Val Cys Leu Cys Glu Cys Val Cys Val His Val Cys Val Cys
785 790 795 800

Thr Ser Val Cys Ile Tyr Val Ser Tyr Thr Ser Lys Gln Ala Gly Gln
805 810 815

Gln

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21

<210> 168
<211> 21
<212> DNA
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<223> Oligonucleotide

<400> 168

tctgagagag tcagtgtcat g

21

<210> 169

<211> 2565

<212> DNA

<213> Homo sapiens

<400> 169

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tggactccaa ttgccttgac agtggtttta gtggctgttg caacattatg taaagaacaa	240
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ttaaaaagac tagaagagat tgaacgtatt ttaaatgggtg aataa 2565

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<211> 733
<212> PRT
<213> Homo sapiens

<400> 170

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Phe Thr Arg Phe Asp Asn Pro Ala Ala Val Ser Pro Thr Pro Thr Arg
35 40 45

Gln Leu Thr Phe Asn Tyr Leu Leu Pro Val Asn Ala Trp Leu Leu Leu
50 55 60

Asn	Pro	Ser	Glu	Leu	Cys	Cys	Asp	Trp	Thr	Met	Gly	Thr	Ile	Pro	Leu
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Ile	Glu	Ser	Leu	Leu	Asp	Ile	Arg	Asn	Leu	Ala	Thr	Phe	Thr	Phe	Phe
			85						90					95	
Cys	Phe	Leu	Gly	Met	Leu	Gly	Val	Phe	Ser	Ile	Arg	Tyr	Ser	Gly	Asp
		100						105					110		
Ser	Ser	Lys	Thr	Val	Leu	Met	Leu	Pro	Ala	Lys	Thr	Asp	Met	Gly	Gln
		115					120					125			
Lys	Phe	Glu	Lys	Ser	Ser	Glu	Asp	Ser	Lys	Gln	Ser	Arg	Arg	Val	Glu
	130					135					140				
Gly	Thr	Phe	Gln	Arg	Asn	Leu	Glu	Ile	Pro	Asn	Ser	Leu	Lys	Asp	Lys
145					150					155					160
Phe	Glu	Leu	Gly	Ala	His	Ala	Phe	Met	Thr	Val	Leu	Ile	Cys	Ser	Ala
				165					170					175	
Leu	Gly	Leu	Ser	Leu	Ala	Val	Arg	Cys	His	Ser	Val	Gly	Phe	Val	Val
			180					185					190		
Ala	Glu	Arg	Val	Leu	Tyr	Val	Pro	Ser	Met	Gly	Phe	Cys	Ile	Leu	Val
		195					200					205			
Ala	His	Gly	Trp	Gln	Lys	Ile	Ser	Thr	Lys	Ser	Val	Phe	Lys	Lys	Leu
	210					215					220				
Ser	Trp	Ile	Cys	Leu	Ser	Met	Val	Ile	Leu	Thr	His	Ser	Leu	Lys	Thr
225					230					235					240
Phe	His	Arg	Asn	Trp	Asp	Trp	Glu	Ser	Glu	Tyr	Thr	Leu	Phe	Met	Ser
				245					250					255	
Ala	Leu	Lys	Val	Asn	Lys	Asn	Asn	Ala	Lys	Leu	Trp	Asn	Asn	Val	Gly
			260					265					270		
His	Ala	Leu	Glu	Asn	Glu	Lys	Asn	Phe	Glu	Arg	Ala	Leu	Lys	Tyr	Phe
		275					280					285			
Leu	Gln	Ala	Thr	His	Val	Gln	Pro	Asp	Asp	Ile	Gly	Ala	His	Met	Asn
	290					295					300				

Val Gly Arg Thr Tyr Lys Asn Leu Asn Arg Thr Lys Glu Ala Glu Glu
 305 310 315 320

Ser Tyr Met Met Ala Lys Ser Leu Met Pro Gln Ile Ile Pro Gly Lys
 325 330 335

Lys Tyr Ala Ala Arg Ile Ala Pro Asn His Leu Asn Val Tyr Ile Asn
 340 345 350

Leu Ala Asn Leu Ile Arg Ala Asn Glu Ser Arg Leu Glu Glu Ala Asp
 355 360 365

Gln Leu Tyr Arg Gln Ala Ile Ser Met Arg Pro Asp Phe Lys Gln Ala
 370 375 380

Tyr Ile Ser Arg Gly Glu Leu Leu Leu Lys Met Asn Lys Pro Leu Lys
 385 390 395 400

Ala Lys Glu Ala Tyr Leu Lys Ala Leu Glu Leu Asp Arg Asn Asn Ala
 405 410 415

Asp Leu Trp Tyr Asn Leu Ala Ile Val His Ile Glu Leu Lys Glu Pro
 420 425 430

Asn Glu Ala Leu Lys Asn Phe Asn Arg Ala Leu Glu Leu Asn Pro Lys
 435 440 445

His Lys Leu Ala Leu Phe Asn Ser Ala Ile Val Met Gln Glu Ser Gly
 450 455 460

Glu Val Lys Leu Arg Pro Glu Ala Arg Lys Arg Leu Leu Ser Tyr Ile
 465 470 475 480

Asn Glu Glu Pro Leu Asp Ala Asn Gly Tyr Phe Asn Leu Gly Met Leu
 485 490 495

Ala Met Asp Asp Lys Lys Asp Asn Glu Ala Glu Ile Trp Met Lys Lys
 500 505 510

Ala Ile Lys Leu Gln Ala Asp Phe Arg Ser Ala Leu Phe Asn Leu Ala
 515 520 525

Leu Leu Tyr Ser Gln Thr Ala Lys Glu Leu Lys Ala Leu Pro Ile Leu
 530 535 540

Glu Glu Leu Leu Arg Tyr Tyr Pro Asp His Ile Lys Gly Leu Ile Leu
 545 550 555 560

Lys Gly Asp Ile Leu Met Asn Gln Lys Lys Asp Ile Leu Gly Ala Lys
 565 570 575

Lys Cys Phe Glu Arg Ile Leu Glu Met Asp Pro Ser Asn Val Gln Gly
 580 585 590

Lys His Asn Leu Cys Val Val Tyr Phe Glu Glu Lys Asp Leu Leu Lys
 595 600 605

Ala Glu Arg Cys Leu Leu Glu Thr Leu Ala Leu Ala Pro His Glu Glu
 610 615 620

Tyr Ile Gln Arg His Leu Asn Ile Val Arg Asp Lys Ile Ser Ser Ser
 625 630 635 640

Ser Phe Ile Glu Pro Ile Phe Pro Thr Ser Lys Ile Ser Ser Val Glu
 645 650 655

Gly Lys Lys Ile Pro Thr Glu Ser Val Lys Glu Ile Arg Gly Glu Ser
 660 665 670

Arg Gln Thr Gln Ile Val Lys Thr Ser Asp Asn Lys Ser Gln Ser Lys
 675 680 685

Ser Asn Lys Gln Leu Gly Lys Asn Gly Asp Glu Glu Thr Pro His Lys
 690 695 700

Thr Thr Lys Asp Ile Lys Glu Ile Glu Lys Lys Arg Val Ala Ala Leu
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Lys Arg Leu Glu Glu Ile Glu Arg Ile Leu Asn Gly Glu
 725 730

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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 171
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<210> 172
 <211> 21
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<220>
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<400> 172
 cgttttctag cttcaggtct g 21

<210> 173
 <211> 3296
 <212> DNA
 <213> Homo sapiens

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 aaggtaaatg ttttaagcaca cagtgaactt cctgaggccc ccaaatactaa tggaactagc 180
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 ggatatttca aagactacta ctattattat taataacaat tgcaatattt gttgagtccc 300
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<210> 174
 <211> 346
 <212> PRT
 <213> Homo sapiens

<400> 174

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Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr
 20 25 30

Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr
 35 40 45

Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr
 50 55 60

Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu
 65 70 75 80

Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val
 85 90 95

Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu
 100 105 110

Ala Ser Phe Thr Tyr Leu Ser Phe Ser Ala Leu Ala His Leu Leu Gln
 115 120 125

Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val
 130 135 140

Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr
 145 150 155 160

Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro
 165 170 175

Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn
180 185 190

Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val
195 200 205

Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg
210 215 220

Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr
225 230 235 240

His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser
245 250 255

Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly
260 265 270

Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala
275 280 285

Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr
290 295 300

Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu
305 310 315 320

Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu
325 330 335

Val Gln Arg Lys Leu Asp Gln Lys Thr Lys
340 345

<210> 175
<211> 2858
<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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<400> 176

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Arg Asp Ser Trp Phe Arg Gly Leu Ile Leu Leu Leu Thr Phe Leu Ile
20           25           30

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Tyr Ala Cys Tyr His Met Ser Arg Lys Pro Ile Ser Ile Val Lys Ser
35           40           45

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Arg Leu His Gln Asn Cys Ser Glu Gln Ile Lys Pro Ile Asn Asp Thr
50           55           60

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His Ser Leu Asn Asp Thr Met Trp Cys Ser Trp Ala Pro Phe Asp Lys
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Asp Asn Tyr Lys Glu Leu Leu Gly Gly Val Asp Asn Ala Phe Leu Ile
85           90           95

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Pro Leu Arg Tyr Tyr Leu Ser Ala Gly Met Leu Leu Ser Gly Leu Phe
 115 120 125

Thr Ser Leu Phe Gly Leu Gly Tyr Phe Trp Asn Ile His Glu Leu Trp
 130 135 140

Tyr Phe Val Val Ile Gln Val Cys Asn Gly Leu Val Gln Thr Thr Gly
 145 150 155 160

Trp Pro Ser Val Val Thr Cys Val Gly Asn Trp Phe Gly Lys Gly Lys
 165 170 175

Arg Gly Phe Ile Met Gly Ile Trp Asn Ser His Thr Ser Val Gly Asn
 180 185 190

Ile Leu Gly Ser Leu Ile Ala Gly Ile Trp Val Asn Gly Gln Trp Gly
 195 200 205

Leu Ser Phe Ile Val Pro Gly Ile Ile Thr Ala Val Met Gly Val Ile
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Thr Phe Leu Phe Leu Ile Glu His Pro Glu Asp Val Asp Cys Ala Pro
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Pro Gln His His Gly Glu Pro Ala Glu Asn Gln Asp Asn Pro Glu Asp
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Pro Gly Asn Ser Pro Cys Ser Ile Arg Glu Ser Gly Leu Glu Thr Val
 260 265 270

Ala Lys Cys Ser Lys Gly Pro Cys Glu Glu Pro Ala Ala Ile Ser Phe
 275 280 285

Phe Gly Ala Leu Arg Ile Pro Gly Val Val Glu Phe Ser Leu Cys Leu
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Leu Phe Ala Lys Leu Val Ser Tyr Thr Phe Leu Tyr Trp Leu Pro Leu
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Tyr Ile Ala Asn Val Ala His Phe Ser Ala Lys Glu Ala Gly Asp Leu
 325 330 335

Ser Thr Leu Phe Asp Val Gly Gly Ile Ile Gly Gly Ile Val Ala Gly
 340 345 350

Leu Val Ser Asp Tyr Thr Asn Gly Arg Ala Thr Thr Cys Cys Val Met
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Asp Gly Ile Ala Ser Ser Ile Val Met Leu Ile Ile Cys Gly Gly Leu
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Val Asn Gly Pro Tyr Ala Leu Ile Thr Thr Ala Val Ser Ala Asp Leu
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Gly Thr His Lys Ser Leu Lys Gly Asn Ala Lys Ala Leu Ser Thr Val
 420 425 430

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Gly Tyr Lys Glu Ile
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<210> 179
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<213> Homo sapiens

<400> 180

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20 25 30

Ala Ile Phe Cys Ser Ser Leu Leu Asp Ser Val Pro Gln Lys Val Glu
35 40 45

Phe Phe Ile Asn Tyr Ser Ser Trp Gly Leu Met Pro Val Gly Phe Asp
50 55 60

Gln Trp Val Thr Pro Ser Val Asp Trp Arg Met Glu Lys Glu Lys Arg
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Leu Gly Tyr Val Ser Pro Pro Leu Phe Leu Leu Leu Ala Gly Phe
85 90 95

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<220>
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<400> 181
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<210> 182
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<400> 182
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<210> 183
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Ser Gln Glu Phe Pro Ala His Glu Gly Arg Gly Asp Glu Glu Arg Pro
20          25          30

```

```

Ile Asp Val Arg Val Val Gln Ala Ala Pro Leu Arg Cys Asp Ser Thr
35          40          45

```

```

Pro Pro Glu Gly Ala Val Gly Asp Ile Cys Lys Lys Glu Asp Ala Gly
50          55          60

```

```

Asn Met Pro Ser Thr Ser Glu Gly Ser Ile Tyr Pro Glu Met Ala His
65          70          75          80

```

```

Phe Leu Arg Asn Lys Leu Ala Gly Ser Ser Val Arg Lys Pro Asp Ser
85          90          95

```

```

Gly Phe Leu Trp Glu Gly Ala Leu Arg Ala Trp Leu Phe Leu Ile Leu
100          105          110

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Ile Val Leu Thr His Ile Met Trp Val Pro Leu Val Gln Val Ser Pro
115          120          125

```

```

Asn Ala Pro Leu Phe His Tyr Ile Glu Ser Ile Ala His Asp Leu Gly
130          135          140

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Pro Pro Ile Gly Ala Ile Phe Leu Leu Ser Ile Ser Trp Ser⁴ Ile Val
 145 150 155 160

Lys Glu Pro Met Ser Arg
 165

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<210> 186
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tccctgctgg ggacaaagtt caactgtaag gagtccccta gaataaacct aaggaaagtc	3600
aggaaagagt aagactgtta agaagaccga agcatgtatt aatgctgtgg ctatgagagg	3660
cctcctgctg cagaaacaca ctccctaca tcaagaagga gtaacttcag gttggatcct	3720
gtgtggatga tcttggtgct aagcagaaaa gaaatttgga ccttgaaacc agcagttcaa	3780
catatatact ttttgcaaaa tttccttgat ttaaaatatt tgttatttta aatatacaaa	3840
acattttaga aaatcttaga gttaaatttta gtcttaaagc cagaaaataa gtttatagcc	3900
atctagatat ttgcatatt gctcttacag caataatggt ttggttcact ttatgaaaaa	3960
taaaatgtat taaaatat	3978

<210> 188
 <211> 1129
 <212> PRT
 <213> Homo sapiens

<400> 188

Met Ala Gly Ile Phe Lys Glu Phe Phe Phe Ser Thr Glu Asp Leu Pro
1 5 10 15

Glu Val Ile Leu Thr Leu Ser Leu Ile Ser Ser Ile Gly Ala Phe Leu
20 25 30

Asn Arg His Leu Glu Asp Phe Pro Ile Pro Val Pro Val Ile Leu Phe
35 40 45

Leu Leu Gly Cys Ser Phe Glu Val Leu Ser Phe Thr Ser Ser Gln Val
50 55 60

Gln Arg Tyr Ala Asn Ala Ile Gln Trp Met Ser Pro Asp Leu Phe Phe
65 70 75 80

Arg Ile Phe Thr Pro Val Val Phe Phe Thr Thr Ala Phe Asp Met Asp
85 90 95

Thr Tyr Met Leu Gln Lys Leu Phe Trp Gln Ile Leu Leu Ile Ser Ile
100 105 110

Pro Gly Phe Leu Val Asn Tyr Ile Leu Val Leu Trp His Leu Ala Ser
115 120 125

Val Asn Gln Leu Leu Leu Lys Pro Thr Gln Trp Leu Leu Phe Ser Ala
130 135 140

Ile Leu Val Ser Ser Asp Pro Met Leu Thr Ala Ala Ala Ile Arg Asp
145 150 155 160

Leu Gly Leu Ser Arg Ser Leu Ile Ser Leu Ile Asn Gly Glu Ser Leu
165 170 175

Met Thr Ser Val Ile Ser Leu Ile Thr Phe Thr Ser Ile Met Asp Phe
180 185 190

Asp Gln Arg Leu Gln Ser Lys Arg Asn His Thr Leu Ala Glu Glu Ile
195 200 205

Val Gly Gly Ile Cys Ser Tyr Ile Ile Ala Ser Phe Leu Phe Gly Ile
210 215 220

Leu Ser Ser Lys Leu Ile Gln Phe Trp Met Ser Thr Val Phe Gly Asp
225 230 235 240

Asp Val Asn His Ile Ser Leu Ile Phe Ser Ile Leu Tyr Leu Ile Phe
245 250 255

Tyr Ile Cys Glu Leu Val Gly Met Ser Gly Ile Phe Thr Leu Ala Ile
260 265 270

Val Gly Leu Leu Leu Asn Ser Thr Ser Phe Lys Ala Ala Ile Glu Glu
275 280 285

Thr Leu Leu Leu Glu Phe Leu Thr Leu Leu Leu Ile Ser Pro Val Leu
290 295 300

Ser Arg Val Gly His Glu Phe Ser Trp Arg Trp Ile Phe Ile Met Val
305 310 315 320

Cys Ser Glu Met Lys Gly Met Pro Asn Ile Asn Met Ala Leu Leu Leu
325 330 335

Ala Tyr Ser Asp Leu Tyr Phe Gly Ser Asp Lys Glu Lys Ser Gln Ile
340 345 350

Leu Phe His Gly Val Leu Val Cys Leu Ile Thr Leu Val Val Asn Arg
355 360 365

Phe Ile Leu Pro Val Ala Val Thr Ile Leu Gly Leu Arg Asp Ala Thr
370 375 380

Ser Thr Lys Tyr Lys Ser Val Cys Cys Thr Phe Gln His Phe Gln Glu
385 390 395 400

Leu Thr Lys Ser Ala Ala Ser Ala Leu Lys Phe Asp Lys Asp Leu Ala
405 410 415

Asn Ala Asp Trp Asn Met Ile Glu Lys Ala Ile Thr Leu Glu Asn Pro
420 425 430

Tyr Met Leu Asn Glu Glu Glu Thr Thr Glu His Gln Lys Val Lys Cys
435 440 445

Pro His Cys Asn Lys Glu Ile Asp Glu Ile Phe Asn Thr Glu Ala Met
450 455 460

Glu Leu Ala Asn Arg Arg Leu Leu Ser Ala Gln Ile Ala Ser Tyr Gln
465 470 475 480

Arg Gln Tyr Arg Asn Glu Ile Leu Ser Gln Ser Ala Val Gln Val Leu
485 490 495

Val Gly Ala Ala Glu Ser Phe Gly Glu Lys Lys Gly Lys Cys Met Ser
500 505 510

Leu Asp Thr Ile Lys Asn Tyr Ser Glu Ser Gln Lys Thr Val Thr Phe
515 520 525

Ala Arg Lys Leu Leu Leu Asn Trp Val Tyr Asn Thr Arg Lys Glu Lys
530 535 540

Glu Gly Pro Ser Lys Tyr Phe Phe Phe Arg Ile Cys His Thr Ile Val
545 550 555 560

Phe Thr Glu Glu Phe Glu His Val Gly Tyr Leu Val Ile Leu Met Asn
565 570 575

Ile Phe Pro Phe Ile Ile Ser Trp Ile Ser Gln Leu Asn Val Ile Tyr
580 585 590

His Ser Glu Leu Lys His Thr Asn Tyr Cys Phe Leu Thr Leu Tyr Ile
595 600 605

Leu Glu Ala Leu Leu Lys Ile Ala Ala Met Arg Lys Asp Phe Phe Ser
610 615 620

His Ala Trp Asn Ile Phe Glu Leu Ala Ile Thr Leu Ile Gly Ile Leu
625 630 635 640

His Val Ile Leu Ile Glu Ile Asp Thr Ile Lys Tyr Ile Phe Asn Glu
645 650 655

Thr Glu Val Ile Val Phe Ile Lys Val Val Gln Phe Phe Arg Ile Leu
660 665 670

Arg Ile Phe Lys Leu Ile Ala Pro Lys Leu Leu Gln Ile Ile Asp Lys
675 680 685

Arg Met Ser His Gln Lys Thr Phe Trp Tyr Gly Ile Leu Lys Gly Tyr
690 695 700

Val Gln Gly Glu Ala Asp Ile Met Thr Ile Ile Asp Gln Ile Thr Ser
705 710 715 720

Ser Lys Gln Ile Lys Gln Met Leu Leu Lys Gln Val Ile Arg Asn Met
725 730 735

Glu His Ala Ile Lys Glu Leu Gly Tyr Leu Glu Tyr Asp His Pro Glu
740 745 750

Ile Ala Val Thr Val Lys Thr Lys Glu Glu Ile Asn Val Met Leu Asn
755 760 765

Met Ala Thr Glu Ile Leu Lys Ala Phe Gly Leu Lys Gly Ile Ile Ser
770 775 780

Lys Thr Glu Gly Ala Gly Ile Asn Lys Leu Ile Met Ala Lys Lys Lys
785 790 795 800

Glu Val Leu Asp Ser Gln Ser Ile Ile Arg Pro Leu Thr Val Glu Glu
805 810 815

Val Leu Tyr His Ile Pro Trp Leu Asp Lys Asn Lys Asp Tyr Ile Asn
820 825 830

Phe Ile Gln Glu Lys Ala Lys Val Val Thr Phe Asp Cys Gly Asn Asp
835 840 845

Ile Phe Glu Glu Gly Asp Glu Pro Lys Gly Ile Tyr Ile Ile Ile Ser
850 855 860

Gly Met Val Lys Leu Glu Lys Ser Lys Pro Gly Leu Gly Ile Asp Gln
865 870 875 880

Met Val Glu Ser Lys Glu Lys Asp Phe Pro Ile Ile Asp Thr Asp Tyr
885 890 895

Met Leu Ser Gly Glu Ile Ile Gly Glu Ile Asn Cys Leu Thr Asn Glu
900 905 910

Pro Met Lys Tyr Ser Ala Thr Cys Lys Thr Val Val Glu Thr Cys Phe
915 920 925

Ile Pro Lys Thr His Leu Tyr Asp Ala Phe Glu Gln Cys Ser Pro Leu
930 935 940

Ile Lys Gln Lys Met Trp Leu Lys Leu Gly Leu Ala Ile Thr Ala Arg
945 950 955 960

Lys Ile Arg Glu His Leu Ser Tyr Glu Asp Trp Asn Tyr Asn Met Gln
965 970 975

Leu Lys Leu Ser Asn Ile Tyr Val Val Asp Ile Pro Met Ser Thr Lys
980 985 990

Thr Asp Ile Tyr Asp Glu Asn Leu Ile Tyr Val Ile Leu Ile His Gly
995 1000 1005

Ala Val Glu Asp Cys Leu Leu Arg Lys Thr Tyr Arg Ala Pro Phe
1010 1015 1020

Leu Ile Pro Ile Thr Cys His Gln Ile Gln Ser Ile Glu Asp Phe
1025 1030 1035

Thr Lys Val Val Ile Ile Gln Thr Pro Ile Asn Met Lys Thr Phe
1040 1045 1050

Arg Arg Asn Ile Arg Lys Phe Val Pro Lys His Lys Ser Tyr Leu
1055 1060 1065

Thr Pro Gly Leu Ile Gly Ser Val Gly Thr Leu Glu Glu Gly Ile
1070 1075 1080

Gln Glu Glu Arg Asn Val Lys Glu Asp Gly Ala His Ser Ala Ala
1085 1090 1095

Thr Ala Arg Ser Pro Gln Pro Cys Ser Leu Leu Gly Thr Lys Phe
1100 1105 1110

Asn Cys Lys Glu Ser Pro Arg Ile Asn Leu Arg Lys Val Arg Lys
1115 1120 1125

Glu

<210> 189
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 189
tttgaaccgg cacttgg

<210> 190
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 190
 tcaaatgcag tagtaaagaa aac 23

<210> 191
 <211> 2898
 <212> DNA
 <213> Homo sapiens

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 ccgtctgtgg tgcgtgaccg cgtgtgtgtt gtgggggcgg ggaaaattca tacaaaagaa 120
 aaaaatatag cacatctctt ggaaatgaaa tacttcaagt ttaatatctc tcttgctaata 180
 gcagaattta tcagccaaga cagctggctg gcctgggtgg ggtttggtta agttgtcaag 240
 tataaggcct actgtaagag ataccaagtg acttttagaa gacagtgtga gggtaaaact 300
 gattactatg cttggaaaca cttagtggta caggataaaa ataagtctaa cacacacaaa 360
 tacagaatga ttatttgtgt gataaatata gataccattt gtgagatggc ttatgcccat 420
 atagaatggg acatgatagt ctgtgcagct tatgcacacg aacttcocaa atacggtgta 480
 aagggttgcc tgacaaatga tgctgcagca tgttgacttg gcctgctgct ggcatgcagg 540
 cttctcagta ggtttggcat ggacaagatc tataaaggcc aagtggaggt aaccagagat 600
 gaatacaacg tgggaagcac tgatggtcag ccagggtgct ttacctgctg tttggatgca 660
 ggccttgcca gaaccaccac tgacaataaa gtttttgggg ctctgagagt gctgtggatg 720
 gaggtttctc tatccctcac agtgcctaac gattccctga gtaaaggga ggcctggccc 780
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 gtgggcagcc agggcgtgga ggcagcagca agcccaaacg gtcaatacgg gccagctgg 900
 ggcctggcgg cggagggcac ggagggagct agggcacagg caccaaagcg ggatttgtcc 960
 tatagcagga ctgactctca cagagactgt tctcctgtct gtcacaacat gtccctgagg 1020
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 aagttttatg agagctgggc cacagccttg ctacagcta tattcccggt gcttggcatc 1140
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cgcctgcctg	cactgcccc	gcctcttggg	ttgacttttag	atgacggtga	agtgatcacc	1440
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tcctgcctcc	acaatgggct	gctatccggg	aacggctgtg	aggtccatta	ccgcagggcg	1560
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ttctacgaag	gagccagccc	cgcagtgaag	ctgattcgaa	gcagttccat	gtatgtggtc	1860
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gacaccagcc	tgtactacct	gcggcaggag	gaggaccggg	cgtggatgta	ttcgcgcacc	1980
caggactgcc	tgcagtacct	gcaggagctg	ctggccttgc	gcaaaaaata	tctcagcagc	2040
ttcagtgatc	tgaagcccca	ccgcacccag	gggatttcc	caacctctc	caaatcctcc	2100
aagggagggg	aaaagactcc	tgtccggtct	actcccaaag	aaataaagaa	agcaacccca	2160
aagaaatact	cgcagttcag	tgtgatgtg	gccgaggcca	ttgccttctt	tgactccatc	2220
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gatgtggact	ttgacgtggc	caccagctcc	agggagcaca	gcttgcatte	taactggatc	2340
ctgcgggcac	cgcgcagaca	ctccgaggat	atcgctgccc	acactgtgca	tactgtagac	2400
ggccagtttc	gaaggagcac	cgagcacagg	accgtgggca	ctcagaggag	actcgagagg	2460
caccccatth	atttgcccaa	ggctgtggaa	ggggccttca	acacctggaa	atttaagccc	2520
aaagcctgca	aaaaagacct	ggggagctcc	agacagatcc	ttttcaactt	ctcaggagaa	2580
gatatggagt	gggatgcaga	gctctttgcg	ttggagcccc	agttgtctcc	tggggaggac	2640
tactatgaga	cagagaaccc	caaaggacag	tggctgcttc	gagaaagact	ttgggagcgg	2700
acgactgggt	ccctgagaag	ctgtccgctt	tcagcgcagc	atgaggtatt	tggtagagtt	2760
gaaaatgcc	attgtaacac	agtcaaccca	ctcagcacac	tgctgctgg	tgccgtgcc	2820
gtgccaaaca	gacctgtggc	ttcccagggg	acaggtctca	ggacactctc	agagcttgag	2880
tttctctg	cg	tgggctga				2898

<211> 965
<212> PRT
<213> Homo sapiens

<400> 192

Met Trp Val Arg Cys Ala Leu Leu Val Ala Arg Asp Cys Gly Cys Ala
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Glu Arg Val Cys Pro Ser Val Val Arg Asp Arg Val Cys Val Val Gly
20 25 30

Ala Gly Lys Ile His Thr Lys Glu Lys Asn Ile Ala His Leu Leu Glu
35 40 45

Met Lys Tyr Phe Lys Phe Asn Ile Ser Leu Ala Asn Ala Glu Phe Ile
50 55 60

Ser Gln Asp Ser Trp Leu Ala Trp Val Gly Phe Val Lys Val Val Lys
65 70 75 80

Tyr Lys Ala Tyr Cys Lys Arg Tyr Gln Val Thr Phe Arg Arg Gln Cys
85 90 95

Glu Gly Lys Thr Asp Tyr Tyr Ala Trp Lys His Leu Val Val Gln Asp
100 105 110

Lys Asn Lys Ser Asn Thr His Lys Tyr Arg Met Ile Ile Cys Val Ile
115 120 125

Asn Thr Asp Thr Ile Cys Glu Met Ala Tyr Ala His Ile Glu Trp Asp
130 135 140

Met Ile Val Cys Ala Ala Tyr Ala His Glu Leu Pro Lys Tyr Gly Val
145 150 155 160

Lys Val Gly Leu Thr Asn Asp Ala Ala Ala Cys Cys Thr Gly Leu Leu
165 170 175

Leu Ala Cys Arg Leu Leu Ser Arg Phe Gly Met Asp Lys Ile Tyr Lys
180 185 190

Gly Gln Val Glu Val Thr Arg Asp Glu Tyr Asn Val Gly Ser Thr Asp
195 200 205

Gly Gln Pro Gly Ala Phe Thr Cys Cys Leu Asp Ala Gly Leu Ala Arg
210 215 220

Thr Thr Thr Asp Asn Lys Val Phe Gly Ala Leu Arg Val Leu Trp Met
 225 230 235 240

Glu Val Ser Leu Ser Leu Thr Val Pro Asn Asp Ser Leu Ser Lys Gly
 245 250 255

Lys Pro Gly Pro Arg Lys Glu Gln Leu Pro Ala Arg Gly Ser Leu Ser
 260 265 270

Arg Gly Val Leu Gly Ala Phe Glu Val Gly Ser Gln Gly Val Glu Ala
 275 280 285

Ala Ala Ser Pro Asn Gly Gln Tyr Gly Pro Ser Trp Gly Leu Ala Ala
 290 295 300

Glu Gly Thr Glu Gly Ala Arg Pro Gln Ala Pro Lys Arg Asp Leu Ser
 305 310 315 320

Tyr Ser Arg Thr Asp Ser His Arg Asp Cys Ser Pro Val Cys His Asn
 325 330 335

Met Ser Leu Arg Gly His Leu Val Pro Lys Lys Pro Ser Lys Glu Lys
 340 345 350

Gln Gly Gln Gln Lys Leu Asp Ser Lys Phe Tyr Glu Ser Trp Ala Thr
 355 360 365

Ala Leu Leu Thr Ala Ile Phe Pro Val Leu Gly Ile Leu Val Leu Val
 370 375 380

Glu Ser Leu Leu Met Asn Asp Pro Met Arg Glu Cys Ile Leu Ser Thr
 385 390 395 400

Ser Gly Phe Ser Gly Pro Arg Ala Arg Leu Leu Gly Val Leu Ala Leu
 405 410 415

Gly Gly Leu Pro Leu His Leu Gly Ala Pro Val Ile Val Met Ala Trp
 420 425 430

Ile Val Leu Ala Leu Leu Phe Thr Arg Ser Arg Thr Arg Ala Asp Pro
 435 440 445

Ala Asp Val Leu Pro Pro Gly Ala Phe Glu Lys Thr Arg Met His Ala
 450 455 460

Leu Pro Pro Pro Leu Gly Leu Thr Leu Asp Asp Gly Glu Val Ile Thr
 465 470 475 480

Thr Arg Leu Leu Thr Asp Ala Ser Val Gln Lys Val Val Val Arg Ile
 485 490 495

Ser Glu Ser Ser Ser Cys Leu His Asn Gly Leu Leu Ser Gly Asn Gly
 500 505 510

Cys Glu Val His Tyr Arg Arg Ala Arg Leu Phe Gln Asp Ala Gln Met
 515 520 525

Pro Ala Gln Ser Pro Ala Tyr Arg Gly Asp Leu Arg Ala Pro Val Asn
 530 535 540

Ala Leu Arg Ile Gln Asn Arg Ser Gln Leu Ser Pro Gly Gly Lys Ile
 545 550 555 560

Lys Trp Arg Gln His Arg Gln Leu Glu Gly Thr His Arg Lys Lys Ser
 565 570 575

Ser Thr Met Phe Arg Lys Ile His Ser Ile Phe Asn Ser Ser Pro Gln
 580 585 590

Arg Lys Thr Ala Ala Glu Ser Pro Phe Tyr Glu Gly Ala Ser Pro Ala
 595 600 605

Val Lys Leu Ile Arg Ser Ser Ser Met Tyr Val Val Gly Asp His Gly
 610 615 620

Glu Lys Phe Ser Glu Ser Leu Lys Lys Tyr Lys Ser Thr Ser Ser Met
 625 630 635 640

Asp Thr Ser Leu Tyr Tyr Leu Arg Gln Glu Glu Asp Arg Ala Trp Met
 645 650 655

Tyr Ser Arg Thr Gln Asp Cys Leu Gln Tyr Leu Gln Glu Leu Leu Ala
 660 665 670

Leu Arg Lys Lys Tyr Leu Ser Ser Phe Ser Asp Leu Lys Pro His Arg
 675 680 685

Thr Gln Gly Ile Ser Ser Thr Ser Ser Lys Ser Ser Lys Gly Gly Lys
 690 695 700

Lys Thr Pro Val Arg Ser Thr Pro Lys Glu Ile Lys Lys Ala Thr Pro
705 710 715 720

Lys Lys Tyr Ser Gln Phe Ser Ala Asp Val Ala Glu Ala Ile Ala Phe
725 730 735

Phe Asp Ser Ile Ile Ala Glu Leu Asp Thr Glu Arg Arg Pro Arg Ala
740 745 750

Ala Glu Ala Ser Leu Pro Asn Glu Asp Val Asp Phe Asp Val Ala Thr
755 760 765

Ser Ser Arg Glu His Ser Leu His Ser Asn Trp Ile Leu Arg Ala Pro
770 775 780

Arg Arg His Ser Glu Asp Ile Ala Ala His Thr Val His Thr Val Asp
785 790 795 800

Gly Gln Phe Arg Arg Ser Thr Glu His Arg Thr Val Gly Thr Gln Arg
805 810 815

Arg Leu Glu Arg His Pro Ile Tyr Leu Pro Lys Ala Val Glu Gly Ala
820 825 830

Phe Asn Thr Trp Lys Phe Lys Pro Lys Ala Cys Lys Lys Asp Leu Gly
835 840 845

Ser Ser Arg Gln Ile Leu Phe Asn Phe Ser Gly Glu Asp Met Glu Trp
850 855 860

Asp Ala Glu Leu Phe Ala Leu Glu Pro Gln Leu Ser Pro Gly Glu Asp
865 870 875 880

Tyr Tyr Glu Thr Glu Asn Pro Lys Gly Gln Trp Leu Leu Arg Glu Arg
885 890 895

Leu Trp Glu Arg Thr Thr Gly Ser Leu Arg Ser Cys Pro Leu Ser Ala
900 905 910

Gln His Glu Val Phe Gly Arg Val Glu Asn Ala Asn Cys Asn Thr Val
915 920 925

Asn Pro Leu Ser Thr Leu Pro Ala Gly Ala Val Pro Val Pro Asn Arg
930 935 940

Pro Val Ala Ser Gln Gly Thr Gly Leu Arg Thr Leu Ser Glu Leu Glu
 945 950 955 960

Phe Leu Cys Val Gly
 965

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 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 193
 cgagaggcac cccatattatt tg 22

<210> 194
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 194
 ttctctgtct catagtagtc ctcccc 26

<210> 195
 <211> 1363
 <212> DNA
 <213> Homo sapiens

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 catccccctct tggagcacta aggaccttcc ctgtgttggg aaaactgtct ggctgtacct 120
 ccaagcctgg ccaaaccctg tgtttgaagg agatgccctg actctgcgat gtcagggatg 180
 gaagaataca ccactgtctc aggtgaagtt ctacagagat ggaaaattcc ttcatttctc 240
 taaggaaaac cagactctgt ccatggggagc agcaacagtg cagagccgtg gccagtacag 300
 ctgctctggg caggtgatgt atattccaca gacattcaca caaacttcag agactgccat 360
 ggttcaagtc caagagctgt ttccacctcc tgtgctgagt gccatccccct ctctgagcc 420
 ccgagagggg agcctggtga ccctgagatg tcagacaaag ctgcaccccc tgaggtcagc 480
 cttgaggctc cttttctcct tccacaagga cggccacacc ttgcaggaca ggggccctca 540
 cccagaactc tgcattcccgg gagccaagga gggagactct gggctttact ggtgtgaggt 600

ggcccctgag ggtggccagg tccagaagca gagccccag ctggaggtca gagtgcaggc 660
 tcctgtatcc cgtcctgtgc tcaactctgca ccacgggcct gctgaccctg ctgtggggga 720
 catggtgcag ctccctctgtg aggcacagag gggctcccct ccgatacctgt attccttcta 780
 ccttgatgag aagattgtgg ggaaccactc agctccctgt ggtggaacca cctccctcct 840
 cttcccagtg aagtcagaac aggatgctgg gaactactcc tgcgaggctg agaacagtgt 900
 ctccagagag aggagtgagc ccaagaagct gtctctgaag ggttctcaag tcttggtcac 960
 tcccgccagc aactggctgg ttccttggct tcctgcgagc ctgcttggcc tgatgggttat 1020
 tgctgctgca cttctgggtt atgtgagatc ctggagaaaa gctgggcccc ttccatccca 1080
 gataccaccc acagctccag gtggagagca gtgccacta tatgccaacg tgcataccca 1140
 gaaagggaaa gatgaagggtg ttgtctactc tgtggtgcat agaacctcaa agaggagtga 1200
 agccaggctc gctgagttca ccgtggggag aaagcacaaa gcttcaccca aattccaccc 1260
 caccctggat ctccacacca agcggctcag ggttaatggt cgagttcagg aagcttatgt 1320
 ggccttggtc aacacctgct cctcacccc cagcctgaag tga 1363

<210> 196
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 196

Met Leu Leu Trp Thr Ala Val Leu Leu Phe Gly Lys Ser Thr Ser Met
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Gly Ile Pro Ser Trp Ser Thr Lys Asp Leu Pro Cys Val Gly Lys Thr
20 25 30

Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp
35 40 45

Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln
50 55 60

Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn
65 70 75 80

Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr
85 90 95

Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr
100 105 110

Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val
115 120 125

Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr
130 135 140

Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu
145 150 155 160

Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro
165 170 175

His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu
180 185 190

Tyr Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser
195 200 205

Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu
210 215 220

Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln
225 230 235 240

Leu Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe
245 250 255

Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly
260 265 270

Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn
275 280 285

Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro
290 295 300

Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser
305 310 315 320

Asn Trp Leu Val Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val
325 330 335

Ile Ala Ala Ala Leu Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly
340 345 350

Pro Leu Pro Ser Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys
 355 360 365

Pro Leu Tyr Ala Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val
 370 375 380

Val Tyr Ser Val Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser
 385 390 395 400

Ala Glu Phe Thr Val Gly Arg Lys His Lys Ala Ser Pro Lys Phe His
 405 410 415

Pro Thr Leu Asp Leu His Thr Lys Arg Leu Arg Val Asn Gly Arg Val
 420 425 430

Gln Glu Ala Tyr Val Ala Leu Val Asn Thr Cys Ser Leu Thr Pro Ser
 435 440 445

Leu Lys
 450

<210> 197
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 197
 gtcagggatg gaagaatac

19

<210> 198
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 198
 acaggaggtg gaaacagc

18

<210> 199
 <211> 534
 <212> DNA
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<400> 199

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acattggtgg gctgcttttag gtatatcaaa attgcttggt tagattctct aatgcacaga 480
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<213> Homo sapiens

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Phe Leu Leu Cys Val Ile Leu Phe Tyr Thr Val Tyr Tyr Val Ser Leu
20 25 30

Ser Met Gly Cys Val Met Phe Glu Val His Glu Leu Asn Val Leu Ala
35 40 45

Pro Phe Asp Phe Lys Thr Asn Pro Ser Trp Leu Asn Ile Asn Tyr Lys
50 55 60

Val Leu Leu Val Ser Thr Glu Val Thr Tyr Phe Val Cys Gly Leu Phe
65 70 75 80

Phe Val Pro Val Val Glu Glu Trp Val Trp Asp Tyr Ala Ile Ser Val
85 90 95

Thr Ile Leu His Val Ala Ile Thr Ser Thr Val Met Leu Glu Phe Pro
100 105 110

Leu Thr Ser His Trp Trp Ala Ala Leu Gly Ile Ser Lys Leu Leu Val
115 120 125

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<400> 201
tcaaacatca cgcagcccat 20

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<220>
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<400> 202
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<210> 203
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<212> DNA
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<213> Homo sapiens

<400> 204

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Tyr Ser Leu Leu Ala Gly Gln Glu Pro Val Tyr Gly Leu Tyr Thr Ser
 20 25 30

Phe Phe Ala Ser Ile Ile Tyr Phe Leu Leu Gly Thr Ser Arg His Ile
 35 40 45

Ser Val Gly Ile Phe Gly Val Leu Cys Leu Met Ile Gly Glu Thr Val
 50 55 60

Asp Arg Glu Leu Gln Lys Ala Gly Tyr Asp Asn Ala His Ser Ala Pro
 65 70 75 80

Ser Leu Gly Met Val Ser Asn Gly Ser Thr Leu Leu Asn His Thr Ser
 85 90 95

Asp Arg Ile Cys Asp Lys Ser Cys Tyr Ala Ile Met Val Gly Ser Thr
 100 105 110

Val Thr Phe Ile Ala Gly Val Tyr Gln
 115 120

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 <212> DNA
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<220>
 <223> Oligonucleotide

<400> 205
 taaatcatatc atcagacagg 20

<210> 206
 <211> 20
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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 206
 aaaacaggta acagcagatt 20

<210> 207
 <211> 513
 <212> DNA
 <213> Homo sapiens

<400> 207

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ggcttccctt tagcaaagcg cctggacgtc atccccctctt cagatacccc aggcctcgtc      180
ctggccactg gcttgactat tgcaggagag cctgataaga tgggacacgg ctccaccttg      240
cattcagcaa gtcgttatcc tgcaactacg atgcaccagg aagaggatgt ggtgaggcca      300
gcttttccat atgcagttag gcatcgaagg gaagatctgc tgtacctaag tgggggtgggc      360
atttcatttt tagggaccgt ctttgttaaa ataatttggg acctcataaa gcctccagcc      420
attcctgatac aggcataagc ttacaacagc agcctggtgc ccataacctg gacagcctgg      480
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<400> 208

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Met Ala Ala Ala Leu Ala Arg Ile Arg Pro Val Gly Leu Gln Ala
1           5           10          15

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Arg Arg Leu Ala Ser Glu Gly Lys Thr Arg Ala Glu Ser Pro Ile Ser
20           25           30

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Asp Pro Ser Asn Ser Tyr Pro Ser Gly Phe Pro Leu Ala Lys Arg Leu
35           40           45

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Asp Val Ile Pro Ser Ser Asp Thr Pro Gly Leu Val Leu Ala Thr Gly
50           55           60

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Leu Thr Ile Ala Gly Glu Pro Asp Lys Met Gly His Gly Ser Thr Leu
65           70           75           80

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His Ser Ala Ser Arg Tyr Pro Ala Thr Thr Met His Gln Glu Glu Asp
85           90           95

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Val Val Arg Pro Ala Phe Pro Tyr Ala Val Arg His Arg Arg Glu Asp
100          105          110

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Leu Leu Tyr Leu Ser Gly Val Gly Ile Ser Phe Leu Gly Thr Val Phe
115          120          125

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Val Lys Ile Ile Trp Asp Leu Ile Lys Pro Pro Ala Ile Pro Asp Gln
130          135          140

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Asp Ile Ala Tyr Asn Ser Ser Leu Val Pro Ile Thr Trp Thr Ala Trp
 145 150 155 160

Ser Glu Val Thr Leu Pro Asp Leu Met Phe
 165 170

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<220>
 <223> Oligonucleotide

<400> 209
 tgagccctag atatacttgg 20

<210> 210
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 210
 cagtcagcct ccatttct 18

<210> 211
 <211> 508
 <212> DNA
 <213> Homo sapiens

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 ttataagga aaatgttttc tagtaccaca cttgtctccc tggaagggat agaagaagga 480
 gggaaggaag tagggaggca gggaagag 508

<210> 212

<211> 97
 <212> PRT
 <213> Homo sapiens

<400> 212

Met Pro Tyr Met Leu Glu Ser Pro Ser Val Cys Gln Ser Val His Thr
 1 5 10 15

Val Arg Gly Ser Gln Lys Trp Arg Leu Thr Glu Gly Arg Ala Asp Ser
 20 25 30

His Leu Ser Ser Leu Leu Tyr Ala His Ala Ser Asn Phe Cys Ser His
 35 40 45

Val Phe Leu Pro Leu Leu Phe Leu Ala Phe Ile Leu Ser Val Ser Leu
 50 55 60

Ser Pro Leu Leu Ala Pro Ser Pro Ser Leu Leu Ser Thr Glu Met Arg
 65 70 75 80

Leu Leu Tyr Leu Ile His Ser Gly Pro Leu Trp Pro Pro Leu Cys Val
 85 90 95

Ser

<210> 213
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 213
 ctgtatttaa tccacagtgg ccccc

25

<210> 214
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 214
 tccctacttc cttccctcct tcttcta

27

<210> 215
 <211> 1321

<212> DNA
 <213> Homo sapiens

<400> 215
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 tgcaggcacc cgtgggaagc tccattcttg tgcagtgcc a ctacaggctc caggatgtca 180
 aagctcagaa ggtgtggtgc cggttcttgc cggaggggtg ccagcccctg gtgtcctcag 240
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<210> 216
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 216

Met Gly Leu Thr Leu Leu Leu Leu Leu Leu Gly Leu Glu Gly Gln
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Gly Ile Val Gly Ser Leu Pro Glu Val Leu Gln Ala Pro Val Gly Ser
20 25 30

Ser Ile Leu Val Gln Cys His Tyr Arg Leu Gln Asp Val Lys Ala Gln
35 40 45

Lys Val Trp Cys Arg Phe Leu Pro Glu Gly Cys Gln Pro Leu Val Ser
50 55 60

Ser Ala Val Asp Arg Arg Ala Pro Ala Gly Arg Arg Thr Phe Leu Thr
65 70 75 80

Asp Leu Gly Gly Gly Leu Leu Gln Val Glu Met Val Thr Leu Gln Glu
85 90 95

Glu Asp Ala Gly Glu Tyr Gly Cys Met Val Asp Gly Ala Arg Gly Pro
100 105 110

Gln Ile Leu His Arg Val Ser Leu Asn Ile Leu Pro Pro Glu Glu Glu
115 120 125

Glu Glu Thr His Lys Ile Gly Ser Leu Ala Glu Asn Ala Phe Ser Asp
130 135 140

Pro Ala Gly Ser Ala Asn Pro Leu Glu Pro Ser Gln Asp Glu Lys Ser
145 150 155 160

Ile Pro Leu Ile Trp Gly Ala Val Leu Leu Val Gly Leu Leu Val Ala
165 170 175

Ala Val Val Leu Phe Ala Val Met Ala Lys Arg Lys Gln Gly Asn Arg
180 185 190

Leu Gly Val Cys Gly Arg Phe Leu Ser Ser Arg Val Ser Gly Met Asn
195 200 205

Pro Ser Ser Val Val His His Val Ser Asp Ser Gly Pro Ala Ala Glu
210 215 220

Leu Pro Leu Asp Val Pro His Ile Arg Leu Asp Ser Pro Pro Ser Phe
225 230 235 240

Asp Asn Thr Thr Tyr Thr Ser Leu Pro Leu Asp Ser Pro Ser Gly Lys
245 250 255

Pro Ser Leu Pro Ala Pro Ser Ser Leu Pro Pro Leu Pro Pro Lys Val
 260 265 270

Leu Val Cys Ser Lys Pro Val Thr Tyr Ala Thr Val Ile Phe Pro Gly
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Gly Asn Lys Gly Gly Gly Thr Ser Cys Gly Pro Ala Gln Asn Pro Pro
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Asn Asn Gln Thr Pro Ser Ser
 305 310

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<220>
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<400> 217
 aggaagaaga agagaccc 18

<210> 218
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<400> 218
 catcacagca aacagcac 18

<210> 219
 <211> 3874
 <212> DNA
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<210> 220

<211> 501
 <212> PRT
 <213> Homo sapiens

<400> 220

Met Arg Ala Glu Glu Pro Cys Ala Pro Gly Ala Pro Ser Ala Leu Gly
 1 5 10 15

Ala Gln Arg Thr Pro Gly Pro Glu Leu Arg Leu Ser Ser Gln Leu Leu
 20 25 30

Pro Glu Leu Cys Thr Phe Val Val Arg Val Leu Phe Tyr Leu Gly Pro
 35 40 45

Val Tyr Leu Ala Gly Tyr Leu Gly Leu Ser Ile Thr Trp Leu Leu Leu
 50 55 60

Gly Ala Leu Leu Trp Met Trp Trp Arg Arg Asn Arg Arg Gly Lys Leu
 65 70 75 80

Gly Arg Leu Ala Ala Ala Phe Glu Phe Leu Asp Asn Glu Arg Glu Phe
 85 90 95

Ile Ser Arg Glu Leu Arg Gly Gln His Leu Pro Ala Trp Ile His Phe
 100 105 110

Pro Asp Val Glu Arg Val Glu Trp Ala Asn Lys Ile Ile Ser Gln Thr
 115 120 125

Trp Pro Tyr Leu Ser Met Ile Met Glu Ser Lys Phe Arg Glu Lys Leu
 130 135 140

Glu Pro Lys Ile Arg Glu Lys Ser Ile His Leu Arg Thr Phe Thr Phe
 145 150 155 160

Thr Lys Leu Tyr Phe Gly Gln Lys Cys Pro Arg Val Asn Gly Val Lys
 165 170 175

Ala His Thr Asn Thr Cys Asn Arg Arg Arg Val Thr Val Asp Leu Gln
 180 185 190

Ile Cys Tyr Ile Gly Asp Cys Glu Ile Ser Val Glu Leu Gln Lys Ile
 195 200 205

Gln Ala Gly Val Asn Gly Ile Gln Leu Gln Gly Thr Leu Arg Val Ile
 210 215 220

Leu Glu Pro Leu Leu Val Asp Lys Pro Phe Val Gly Ala Val Thr Val
 225 230 235 240

Phe Phe Leu Gln Lys Gln His Leu Gln Ile Asn Trp Thr Gly Leu Thr
 245 250 255

Asn Leu Leu Asp Ala Pro Gly Ile Asn Asp Val Ser Asp Ser Leu Leu
 260 265 270

Glu Asp Leu Ile Ala Thr His Leu Val Leu Pro Asn Arg Val Thr Val
 275 280 285

Pro Val Lys Lys Gly Leu Asp Leu Thr Asn Leu Arg Phe Pro Leu Pro
 290 295 300

Cys Gly Val Ile Arg Val His Leu Leu Glu Ala Glu Gln Leu Ala Gln
 305 310 315 320

Lys Asp Asn Phe Leu Gly Leu Arg Gly Lys Ser Asp Pro Tyr Ala Lys
 325 330 335

Val Ser Ile Gly Leu Gln His Phe Arg Ser Arg Thr Ile Tyr Arg Asn
 340 345 350

Leu Asn Pro Thr Trp Asn Glu Val Phe Glu Phe Met Val Tyr Glu Val
 355 360 365

Pro Gly Gln Asp Leu Glu Val Asp Leu Tyr Asp Glu Asp Thr Asp Arg
 370 375 380

Asp Asp Phe Leu Gly Ser Leu Gln Ile Cys Leu Gly Asp Val Met Thr
 385 390 395 400

Asn Arg Val Val Asp Glu Trp Phe Val Leu Asn Asp Thr Thr Ser Gly
 405 410 415

Arg Leu His Leu Arg Leu Glu Trp Leu Ser Leu Leu Thr Asp Gln Glu
 420 425 430

Val Leu Thr Glu Asp His Gly Gly Leu Ser Thr Ala Ile Leu Val Val
 435 440 445

Phe Leu Glu Ser Ala Cys Asn Leu Pro Arg Asn Pro Phe Asp Tyr Leu
 450 455 460

Asn Gly Glu Tyr Arg Ala Lys Lys Leu Ser Arg Phe Ala Arg Val Lys
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Gln Gly Gln Gln Arg Pro Phe Phe Leu Cys Gln Thr Ile Cys Arg Gln
 485 490 495

Glu Asp Thr Tyr Lys
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<220>
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<210> 222
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<220>
 <223> Oligonucleotide

<400> 222
 tcttggtggc ccactcgac 19

<210> 223
 <211> 1020
 <212> DNA
 <213> Homo sapiens

<400> 223
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 tccttaaaaa gtagcacttt gaagcctact attgaagcat tgcctaattgt gctaccttta 180
 aatgaagatg ttaataagca ggaagaaaag aatgaagatc atactcccaa ttatgctcct 240
 gctaattgaga aaaatggcaa ttattataaa gatataaaac aatatgtgtt cacaacacaa 300
 aatccaaatg gcactgagtc tgaaatatct gtgagagcca caactgacct gaattttgct 360
 ctaaaaaacg ataaaactgt caatgcaact acatatgaaa aatccaccat tgaagaagaa 420
 acaactacta gcgaaccctc tcataaaaat attcaaagat caaccccaaa cgtgcctgca 480

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ttttggacaa tgtagctaa agctataaat ggaacagcag tggatcatgga .tgataaagat 540
caattatttc acccaattcc agagtctgat gtgaatgcta cacagggaga aaatcagcca 600
gatctagagg atctgaagat caaaataatg ctgggaatct cgttgatgac cctcctcctc 660
tttgtggtcc tcttggcatt ctgtagtgct aactgtaca aactgaggca tctgagttat 720
aaaagttgtg agagtcaagta ctctgtcaac ccagagctgg ccacgatgtc ttactttcat 780
ccatcagaag gtgtttcaga tacatccttt tccaagagtg cagagagcag cacatttttg 840
ggtaccactt cttcagatat gagaagatca ggcacaagaa catcagaatc taagataatg 900
acggatatca tttccatagg ctcagataat gagatgcatg aaaacgatga gtcggttacc 960
cgggtgaagaa atcaaggaac ccggtgaaga aatcttattg atgaataaat aactttaatt 1020

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<210> 224
<211> 294
<212> PRT
<213> Homo sapiens

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<400> 224

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Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
1           5           10           15

```

```

Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
          20          25          30

```

```

Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
          35          40          45

```

```

Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
          50          55          60

```

```

Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
65          70          75          80

```

```

Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
          85          90          95

```

```

Asp Lys Thr Val Asn Ala Thr Thr Tyr Glu Lys Ser Thr Ile Glu Glu
          100          105          110

```

```

Glu Thr Thr Thr Ser Glu Pro Ser His Lys Asn Ile Gln Arg Ser Thr
          115          120          125

```

```

Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala Ile Asn Gly
          130          135          140

```

Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His Pro Ile Pro
 145 150 155 160

Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro Asp Leu Glu
 165 170 175

Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met Thr Leu Leu
 180 185 190

Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu Tyr Lys Leu
 195 200 205

Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser Val Asn Pro
 210 215 220

Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly Val Ser Asp
 225 230 235 240

Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu Gly Thr Thr
 245 250 255

Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu Ser Lys Ile
 260 265 270

Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met His Glu Asn
 275 280 285

Asp Glu Ser Val Thr Arg
 290

<210> 225
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 225
 tgaatgctac acagggagaa aatc

24

<210> 226
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 226

tgaaagtaag acatcgtggc c

21

<210> 227

<211> 309

<212> DNA

<213> Homo sapiens

<400> 227

atgaccacag ccacccctct gggggatacc accttcttct cactgaacat gaccaccagg 60

ggagaagact tctgtataa gagttctgga gccattgttg ctgccgttgt ggtggttgtc 120

atcatcatct tcaccgtggt tctgatcctg ctgaagatgt acaacaggaa aatgaggacg 180

aggcggaac tagagcccaa gggccccaag ccaaccgcc cttctgccgt gggcccaaac 240

agcaacggca gccaacaccc agcaactgtg accttcagtc ctgttgacgt ccaggtggag 300

acgcgatga 309

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Thr Thr Ala Thr Pro Leu Gly Asp Thr Thr Phe Phe Ser Leu Asn
1 5 10 15

Met Thr Thr Arg Gly Glu Asp Phe Leu Tyr Lys Ser Ser Gly Ala Ile
20 25 30

Val Ala Ala Val Val Val Val Val Ile Ile Ile Phe Thr Val Val Leu
35 40 45

Ile Leu Leu Lys Met Tyr Asn Arg Lys Met Arg Thr Arg Arg Glu Leu
50 55 60

Glu Pro Lys Gly Pro Lys Pro Thr Ala Pro Ser Ala Val Gly Pro Asn
65 70 75 80

Ser Asn Gly Ser Gln His Pro Ala Thr Val Thr Phe Ser Pro Val Asp
85 90 95

Val Gln Val Glu Thr Arg
100

<210> 229
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 229
 ggggatacca ccttcttct 19

<210> 230
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 230
 agttgctggg tgttggt 18

<210> 231
 <211> 2510
 <212> DNA
 <213> Homo sapiens

<400> 231
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 gtcttctttt aagaagtgtc tgttcatatc ctttgccctt tcgcttctat gcaccaataa 180
 caccaggt gagagtcaaa ccaagaacac aatcctgact acagtagcca taaagaaaat 240
 gaaatacctg ggaatacacc taatcaaaaa catgaaagca ctctctagag ggagaactac 300
 aaaacattgc tgaaagaaat cagagatgat tctctgaaaa agaagtcaga ttagaaatga 360
 ttctctgaaa aagaaatcat ctctgatttc tttcagcagt gtgttttttg tttgtttgtt 420
 tgttttgaga cagagtcttg ctctgtcgcc aaggctggag ggcaatggca tgatttcagc 480
 tcaactaac ctctgctcc tgggttcgag cgattctcct acctcagcct cccgagtagc 540
 tgggattaca ggaggctgag aaaatgttag aaattggggg agacaagttt cccttagaga 600
 gcaggaagtt actaagtagt cctggaaaga acatcagttg cagatgtgac ccctctgaga 660
 ttaatatatc tgatgaaatg cctaaaacta cagtttgga agctctcagt atgaattctg 720
 gaaatgcaaa ggaaaagagt ctcttcaact aagagtcttt gctgggatgg aagatttggg 780
 ccgtgtggtg cctcagggaa gttctggtta cagagaaaat ggcgagtctc tcagagaaga 840
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attcttgggtg tgcattggaa ggcattccagc tatccccata ccagcagcca gtcaccagat	960
gtgaatgtgg aagcagaaga ccacctcctg ttggttcttc tctcttctct tctttttctc	1020
tttagaacgg ccaccattga agacctagct tcccattttc cagacgtttt ctctgaaatt	1080
ctctgctggc ctgccaagcc atatggattc attctgccac tgaggagtcc ttcagtgagg	1140
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gctctccagt gctcttagtg tctacaggct cctaggcagc cctgggcctt ggtttgatta	1260
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tgagtttaga ttgcaacaga aggaattagt ttagatacca ggaagaactt cctagcctga	1620
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gaatagaaag gaggatatga tgtttttatt ggccattttg cgggactctt cgacttcttg	1740
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tgtctcctta gctgccttag agtaaacgat catcagttca atggacccaa atcaccttca	1860
gccatgtggg ttcttcatca tcatggattt cttttggttg acaaacattc tggtctcag	1920
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ttaaaactac atttatagtt tttctcttct cttctatggt gcaatgaatg taaagtattt	2040
gggatccagt gcttataaac ctttccttcc tttgtgcaca gaatgtaact agcaagccca	2100
ttagcaccca gataattcta tcatgttagt tcccatcct ggaaaatctt tgtacagtgg	2160
gaagttcccc gatgtgtttt tctttcttag gtgaagggtt ggctatatca ctttattgaa	2220
ttttgcattc cttagacttt taaaatatac taatgtattc tagtcttact ctaaagacct	2280
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ctcagaaggg atgcctgctg taaacaagca gtatgtatgg ttgtaccaat gcctattggc	2460
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<210> 232
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 232

Met Gln Arg Lys Arg Val Ser Ser Thr Lys Ser Leu Cys Trp Asp Gly
1 5 10 15

Arg Phe Gly Pro Cys Gly Ala Ser Gly Lys Phe Trp Leu Gln Arg Lys
20 25 30

Trp Arg Val Ser Gln Arg Arg Ser Lys Thr Lys Ser Gly Pro Val Leu
35 40 45

Gly His Leu Lys Ala Met Pro Lys His Ser Val Ile Leu Gly Val His
50 55 60

Trp Lys Ala Ser Ser Tyr Pro His Thr Ser Ser Gln Ser Pro Asp Val
65 70 75 80

Asn Val Glu Ala Glu Asp His Leu Leu Leu Val Leu Leu Leu Phe Leu
85 90 95

Leu Phe Leu Phe Arg Thr Ala Thr Ile Glu Asp Leu Ala Ser His Phe
100 105 110

Pro Asp Val Phe Ser Glu Ile Leu Cys Trp Pro Ala Lys Pro Tyr Gly
115 120 125

Phe Ile Leu Pro Leu Arg Ser Pro Ser Val Arg Ser Leu Phe Leu Lys
130 135 140

Asp Arg Val Gly Ser Arg Arg Gly Thr Glu Arg Thr Ser Ser Leu Ala
145 150 155 160

Leu Gln Cys Ser

<210> 233

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 233

gaggctgaga aaatgtaga

20

<210> 234

<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 234
tccatcccag caaagact 18

<210> 235
<211> 1977
<212> DNA
<213> Homo sapiens

<400> 235
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tcctgtgaga aacactcatt tgattgtgaa aagacttgaa ttctatgcta agcaggggttc 180
caagtagcta aatgaatgat ctcagcaagt ctctcttgct gctgctgcta ctcgtttaca 240
tttattgatt acttacgatg attcaggtac tgttgtaagt gctttacatg ctgttatacg 300
agactcttgg gagaaatcac tttaatgaag cttgagacac atggcattgc catgcaatga 360
tttttcccc ctcttcacgg gatcagaggg aactaataga atgtgacaat gattcttttag 420
cagggactgc tgaggcttct ggttcctttt taagatctgc agtgaaaagaa gatgagaaac 480
atggatatgc ccttcttttg gtccccctct tcctttatct gatctctact tccttctata 540
aatatattag ggctacattg tccctttgta tttcaaacaa ggcaaaaaga ggttgtaatt 600
acactttact gcaatcctca gtttctccag ggaacaggaa tgcaaaggct ttgaaggcct 660
ctctatctgc tgacatggtc agctgggtgc catgggccaa gtccttctgt tgccctctc 720
tgtcaccaag taagctaggt cctttctgag gctcagggtt gctgtgatga tgatcacttt 780
taggcagaag gttagaggcc tcatgagtgc tatatggact ttattaggct ttagatttga 840
tggggaataa gggatgtgat ttgtcttttg ggaactcatc tttgattcat cattgtctct 900
tggtatcttg gaatttccat gtcattacag tctacagaat gaaagagtaa cctgtcccag 960
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cttagccagt gactcattcc agaaccagaa ccttggtgaa atctcaaccg acaccagaga 1380
 tcggtgtctt cagtcctaga ctgatggaga aaatccagaa tatatactag aagctccaaa 1440
 tgctctgggt ttcagctcct ctgtgctgtg gacactgact ttggctcaga actccgattt 1500
 agtacaaaag gctcattttt atttcagggg cactcttctt aaagcaaacc taataaatga 1560
 aatatggaat tcacagatac acacacacat taaaaaatta acctagtgtg tctgtgagga 1620
 gtaggcagaa attcactgtg taaaagaatg cttcatttca tagagaattt gtgttaagat 1680
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 gtttatgtaa gtggaaaaag catgttgcaa aataacttgg tgtctatgat tcagtttatg 1800
 taaaataata aatgtatgtg ggaatacgtg tgttgaaaga tgtacatcaa tttgctaaca 1860
 atggttatct ctgacgtggg gggatttgag atgtgttttt ctttttggtt gtatttttct 1920
 ctattgtttg acttaacaca gaacatgttt gggtacaaca ataaagttat tgaagac 1977

<210> 236
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 236

Met Ile Phe Pro Pro Ser Ser Arg Asp Gln Arg Glu Leu Ile Glu Cys
 1 5 10 15

Asp Asn Asp Ser Leu Ala Gly Thr Ala Glu Ala Ser Gly Ser Phe Leu
 20 25 30

Arg Ser Ala Val Lys Glu Asp Glu Lys His Gly Tyr Ala Leu Leu Leu
 35 40 45

Val Pro Leu Phe Leu Tyr Leu Ile Ser Thr Ser Phe Tyr Lys Tyr Ile
 50 55 60

Arg Ala Thr Leu Ser Leu Cys Ile Ser Asn Lys Ala Lys Arg Gly Cys
 65 70 75 80

Asn Tyr Thr Leu Leu Gln Ser Ser Val Ser Pro Gly Asn Arg Asn Ala
 85 90 95

Lys Ala Leu Lys Ala Ser Leu Phe Ala Asp Met Val Ser Trp Val Pro
 100 105 110

Trp Ala Lys Ser Phe Cys Cys Pro Pro Leu Ser Pro Ser Lys Leu Gly
 115 120 125

Pro Phe
130

<210> 237
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 237
atgattcttt agcagggga 18

<210> 238
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 238
ctcttttttgc cttgtttg 18

<210> 239
<211> 1293
<212> DNA
<213> Homo sapiens

<400> 239
aggccgaggg gttcggcgac gcggagggag ggagagtctg ggccgcgcgg gagccgcagg 60
gcgccctagc cttcgcagaa acgatggcgg aggaagaagg accacctgta gagctgcgcc 120
aaagaaaaaa gccaaagtct tcagaaaata aggaatctgc caaagaagag aaaatcagtg 180
acattccaat tcctgaaaga gctccaaaac atgtattatt tcaacgcttt gcaaagattt 240
tcattggctg tcttgcagcg gttactagtg gtatgatgta tgctctctac ttatcagcat 300
accatgaacg gaaattctgg ttttccaaca ggcaggagct tgaacgggaa atcacgtttc 360
agggtgacag tgccatttat tactcctatt ataaagatat gttaaaggca ccttcatttg 420
aaagaggtgt ttacgaactg acacacaata acaaaactgt atctctgaag actataaatg 480
cagtgcagca aatgtctctg tatccggaac ttattgctag cattttatat caagccactg 540
gtagcaatga gattattgag ccagtgtatt tctatattgg cattgttttt ggattgcaag 600
gaatatatgt tactgcttta tttgttaca gttggcttat gagtgggaaca tggctagcag 660
gaatgcttac tgttgcgtgg ttcgttatta acagttgcac agacccttgg tacagtgtgg 720

gaggtgacaa cacaggatat taataccagg aggcaggaat cattgggacc gtcttggagg 780
ctggctacca cattcaatta actttgctat taatttcatg taatccctat atctgtcttc 840
atatttgaag aggaaaagat actttctcat gtaaacataa tggttttaaa gaataagact 900
ctcttatgct acttaaaciaa aagaataaga ctctcttttag agatcttagt gagaattgta 960
agaaataaaa taaacagaag tctgactgcc ttatttgatg tcaactgatgt atgttgatt 1020
gctggagtag aagttaaata gaaaaattga cctggatat tctactcaaa tgtatctttt 1080
gacaattgaa atgttcttaa tagctaagtt ttaaaaaatg cgtttgtttg ctttttgttt 1140
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aaaaagatat taaagtcatt ccattatatt atg 1293

<210> 240
<211> 219
<212> PRT
<213> Homo sapiens

<400> 240

Met Ala Glu Glu Glu Gly Pro Pro Val Glu Leu Arg Gln Arg Lys Lys
1 5 10 15

Pro Lys Ser Ser Glu Asn Lys Glu Ser Ala Lys Glu Glu Lys Ile Ser
20 25 30

Asp Ile Pro Ile Pro Glu Arg Ala Pro Lys His Val Leu Phe Gln Arg
35 40 45

Phe Ala Lys Ile Phe Ile Gly Cys Leu Ala Ala Val Thr Ser Gly Met
50 55 60

Met Tyr Ala Leu Tyr Leu Ser Ala Tyr His Glu Arg Lys Phe Trp Phe
65 70 75 80

Ser Asn Arg Gln Glu Leu Glu Arg Glu Ile Thr Phe Gln Gly Asp Ser
85 90 95

Ala Ile Tyr Tyr Ser Tyr Tyr Lys Asp Met Leu Lys Ala Pro Ser Phe
100 105 110

Glu Arg Gly Val Tyr Glu Leu Thr His Asn Asn Lys Thr Val Ser Leu
115 120 125

Lys Thr Ile Asn Ala Val Gln Gln Met Ser Leu Tyr Pro Glu Leu Ile
 130 135 140

Ala Ser Ile Leu Tyr Gln Ala Thr Gly Ser Asn Glu Ile Ile Glu Pro
 145 150 155 160

Val Tyr Phe Tyr Ile Gly Ile Val Phe Gly Leu Gln Gly Ile Tyr Val
 165 170 175

Thr Ala Leu Phe Val Thr Ser Trp Leu Met Ser Gly Thr Trp Leu Ala
 180 185 190

Gly Met Leu Thr Val Ala Trp Phe Val Ile Asn Ser Cys Thr Asp Pro
 195 200 205

Trp Tyr Ser Val Gly Gly Asp Asn Thr Gly Tyr
 210 215

<210> 241
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 241
 accgctgcaa gacagccaa 19

<210> 242
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 242
 gcagaaacga tggcggagga 20

<210> 243
 <211> 1291
 <212> DNA
 <213> Homo sapiens

<400> 243
 atcatgtatt ccattgccac tggaggcttg gttttgatgg cagtgtttta tacacagaaa 60

gacagctgca tggaaaacaa aattctgctg ggagtaaatg gaggcctgtg cctgcttata 120

tcattggtag ccattctacc ctgggtccaa aatcgacagc cacactcggg gctcttataa 180

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tcaggggtca taagctgcta tgtcacctac ctcaccttct cagctctgtc cagcaaacct 240
gcagaagtag ttctagatga acatgggaaa aatgttacaa tctgtgtgcc tgacttttgt 300
caagacctgt acagagatga aaacttggtg actatactgg ggaccagcct cttaatcgga 360
tgtatcttgt attcatgttt gacatcaaca acaagatcga gttctgacgc tctgcagggg 420
cgatacgcag ctctgaatt ggagatagct cgctgttggt tttgcttcag tcctggtgga 480
gaggacactg aagagcagca gccggggaag gagggaccac gggtcattta tgacgagaag 540
aaaggcaccg tctacatcta ctctacttc cacttcgtgt tcttcctagc ttccctgtat 600
gtgatgatga ccgtcaccaa ctgggtcaac tacgaaagtg ccaacatcga gagcttcttc 660
agcgggagct ggtccatctt ctgggtcaag atggcctcct gctggatatg cgtgctgttg 720
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gaaaaaaaaa aatctcctga ttagcttttt acttttgaaa ttcaaaaaga aactaccagt 960
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gggcacagca tcttttcaca gggataaaaa tatcttgtgg ggccagtcac tctcatcctc 1140
ggaatagaaa aacatgccaa aatcttgagt cccagcgcc taacagaatc cagaccctc 1200
tcactcactt ccgcctctta gagccttgtc ccagggggc tttgaggaca ggactcagcc 1260
tgcagggcc cttggtattta tagggcca g 1291

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<210> 244
<211> 257
<212> PRT
<213> Homo sapiens

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<400> 244

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Met Tyr Ser Ile Ala Thr Gly Gly Leu Val Leu Met Ala Val Phe Tyr
1           5           10          15

```

```

Thr Gln Lys Asp Ser Cys Met Glu Asn Lys Ile Leu Leu Gly Val Asn
20           25           30

```

```

Gly Gly Leu Cys Leu Leu Ile Ser Leu Val Ala Ile Ser Pro Trp Val
35           40           45

```

```

Gln Asn Arg Gln Pro His Ser Gly Leu Leu Gln Ser Gly Val Ile Ser
50           55           60

```

Cys Tyr Val Thr Tyr Leu Thr Phe Ser Ala Leu Ser Ser Lys Pro Ala
65 70 75 80

Glu Val Val Leu Asp Glu His Gly Lys Asn Val Thr Ile Cys Val Pro
85 90 95

Asp Phe Gly Gln Asp Leu Tyr Arg Asp Glu Asn Leu Val Thr Ile Leu
100 105 110

Gly Thr Ser Leu Leu Ile Gly Cys Ile Leu Tyr Ser Cys Leu Thr Ser
115 120 125

Thr Thr Arg Ser Ser Ser Asp Ala Leu Gln Gly Arg Tyr Ala Ala Pro
130 135 140

Glu Leu Glu Ile Ala Arg Cys Cys Phe Cys Phe Ser Pro Gly Gly Glu
145 150 155 160

Asp Thr Glu Glu Gln Gln Pro Gly Lys Glu Gly Pro Arg Val Ile Tyr
165 170 175

Asp Glu Lys Lys Gly Thr Val Tyr Ile Tyr Ser Tyr Phe His Phe Val
180 185 190

Phe Phe Leu Ala Ser Leu Tyr Val Met Met Thr Val Thr Asn Trp Phe
195 200 205

Asn Tyr Glu Ser Ala Asn Ile Glu Ser Phe Phe Ser Gly Ser Trp Ser
210 215 220

Ile Phe Trp Val Lys Met Ala Ser Cys Trp Ile Cys Val Leu Leu Tyr
225 230 235 240

Leu Cys Thr Leu Val Ala Pro Leu Cys Cys Pro Thr Arg Glu Phe Ser
245 250 255

Val

<210> 245
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 245

agtcaggcac acagattg

18

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<211> 18

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<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 246

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18

<210> 247

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 247

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gggggaggag gaggggagct aggtggtgac atcacagtcg aagggtataa aagcttccag 180

ccaaacggca ttgaagttga agatacaacc tgacagcaca gcctgagatc ttgggggatcc 240

ctcagcctaa caccacaga cgtcagctgg tggattcccg ctgcatcaag gcctaccac 300

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cagagctcag cccttgcccc ctcaagactt tgaagaagag gaggcagatg agactgagac 420

ggcgtggccg cctttgccgg ctgtcccctg cgactacgac cactgccgac acctgcaggt 480

gccctgcaag gagctacaga gggtcgggcc ggcggcctgc ctgtgcccag gactctccag 540

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ccgcgcagtg gtccactggg gtgccccctt ctccccggtc ctccactact ggctgctgct 660

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ttaaaaggaa gt 2412

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<210> 248
<211> 238
<212> PRT
<213> Homo sapiens

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<400> 248

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Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe Leu
1           5           10           15

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Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu Glu Glu
20           25           30

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Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala Val Pro Cys
 35 40 45

Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys Lys Glu Leu Gln
 50 55 60

Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly Leu Ser Ser Pro Ala
 65 70 75 80

Gln Pro Pro Asp Pro Pro Arg Met Gly Glu Val Arg Ile Ala Ala Glu
 85 90 95

Glu Gly Arg Ala Val Val His Trp Cys Ala Pro Phe Ser Pro Val Leu
 100 105 110

His Tyr Trp Leu Leu Leu Trp Asp Gly Ser Glu Ala Ala Gln Lys Gly
 115 120 125

Pro Pro Leu Asn Ala Thr Val Arg Arg Ala Glu Leu Lys Gly Leu Lys
 130 135 140

Pro Gly Gly Ile Tyr Val Val Cys Val Val Ala Ala Asn Glu Ala Gly
 145 150 155 160

Ala Ser Arg Val Pro Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp
 165 170 175

Ile Pro Ala Phe Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro
 180 185 190

Arg Thr Leu Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu
 195 200 205

Leu Ser Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp
 210 215 220

Gly Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
 225 230 235

<210> 249

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 249

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18

<210> 250

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 250

gccgtctcag tctcatct

18

<210> 251

<211> 1024

<212> DNA

<213> Homo sapiens

<400> 251

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ggacaagcgg gcagcatgct cagggcggtc gggagcctac tgcgccttgg ccgcggggcta 180

acagtccgct gcggccccgg ggcgcctctc gaggccacgc gacggccccgc accggctctt 240

ccgccccggg gtctcccttg ctactccagc ggcggggccc ccagcaattc tgggccccaa 300

ggtcacgggg agattcaccg agtccccacg cagcgcaggc cttcgagtt cgacaagaaa 360

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<210> 252
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 252

Met Leu Arg Ala Val Gly Ser Leu Leu Arg Leu Gly Arg Gly Leu Thr
 1 5 10 15

Val Arg Cys Gly Pro Gly Ala Pro Leu Glu Ala Thr Arg Arg Pro Ala
 20 25 30

Pro Ala Leu Pro Pro Arg Gly Leu Pro Cys Tyr Ser Ser Gly Gly Ala
 35 40 45

Pro Ser Asn Ser Gly Pro Gln Gly His Gly Glu Ile His Arg Val Pro
 50 55 60

Thr Gln Arg Arg Pro Ser Gln Phe Asp Lys Lys Ile Leu Leu Trp Thr
 65 70 75 80

Gly Arg Phe Lys Ser Met Glu Glu Ile Pro Pro Arg Ile Pro Pro Glu
 85 90 95

Met Ile Asp Thr Ala Arg Asn Lys Ala Arg Val Lys Ala Cys Tyr Ile
 100 105 110

Met Ile Gly Leu Thr Ile Ile Ala Cys Phe Ala Val Ile Val Ser Ala
 115 120 125

Lys Arg Ala Val Glu Arg His Glu Ser Leu Thr Ser Trp Asn Leu Ala
 130 135 140

Lys Lys Ala Lys Trp Arg Glu Glu Ala Ala Leu Ala Ala Gln Ala Lys
 145 150 155 160

Ala Lys

<210> 253
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 253
attatcgct gctttgctg 19

<210> 254
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 254
ttcccatctt ctactgttgc tg 22

<210> 255
<211> 852
<212> DNA
<213> Homo sapiens

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<211> 110
<212> PRT
<213> Homo sapiens

<400> 256

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Pro Ser Pro Gln Val Leu Leu Leu Leu Leu Arg Glu Ala Pro Ser Thr
 20 25 30

Ala Ala Ala Val Ala Gly Trp Leu Val Val Ala Ser Met Ala Leu Leu
 35 40 45

Gln Leu His Ala Val Gly Gly Val Ala Leu Thr Ser Ser His Pro Ser
 50 55 60

Met Trp Ala Thr Gly Glu Glu Leu Arg Lys Pro Pro Trp Gln Gly Ser
 65 70 75 80

Ala Gly Ser Ala Ser Gly Val Glu Glu Leu Thr Gly Lys His Ser Cys
 85 90 95

Pro Gly Pro Glu Glu Pro Ala Thr Val Gln Lys Ala Pro Ala
 100 105 110

<210> 257
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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 257
 ttgctgttcc cattcata 18

<210> 258
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 <212> DNA
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<220>
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<400> 258
 gataaagtct ggttcctcc 19

<210> 259
 <211> 4231
 <212> DNA
 <213> Homo sapiens

<400> 259
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<210> 260
<211> 359
<212> PRT
<213> Homo sapiens

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<400> 260

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Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
20 25 30

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Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
35 40 45

```

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Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
50 55 60

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Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
65 70 75 80

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Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
85 90 95

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Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
100 105 110

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Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
115 120 125

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Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
 130 135 140

Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg
 145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe
 165 170 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val
 180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile
 195 200 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu
 210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala
 225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val
 245 250 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr
 260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
 275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
 290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
 305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
 325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350

Gln Arg Gln Glu Ser Val Phe
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<220>
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<400> 261
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<210> 262
 <211> 18
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<220>
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<400> 262
 accagcgagt acaccacg 18

<210> 263
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<210> 264
 <211> 171
 <212> PRT
 <213> Homo sapiens

<400> 264

Met Thr Glu Glu Thr Arg Ile Val Tyr Trp Ile Lys Asp Arg Gln Leu
1 5 10 15

Thr Asn Arg Asp Ser Thr Ile Leu Glu Leu Gln Lys Val Leu Lys Thr
20 25 30

Cys Cys Ala Gln Ser Met Lys Ile Phe Cys Cys Leu Trp Asn Phe Val
35 40 45

Tyr Lys Gln Leu Glu Asp Ala Ala Gln Gly Leu Thr Met Gly Gly Asp
50 55 60

Val Glu Glu His Glu Asp Leu Thr Ala Asp Ser Thr Ile Phe Lys Phe
65 70 75 80

Val Glu Ala Tyr Thr Glu Trp Glu Val Lys Arg Trp Ser Asp Asn Asn
85 90 95

Leu Ile Met Lys Gln Thr Asn Val Lys Arg Arg Arg Leu Asp Asp Val
100 105 110

Gly Pro Glu Leu Glu Lys Ala Val Trp Glu Leu Gly Cys Pro Pro Ser
115 120 125

Ile Gln Cys Leu Leu Pro Pro Val Cys Tyr Ala Cys Val Trp Phe Phe
130 135 140

Gln Val Leu Ile Phe Phe Leu Ile Leu Ser Phe Cys Gly Tyr Ile Val
145 150 155 160

Gly Val Tyr Ile Tyr Gly Leu His Glu Met Phe
165 170

<210> 265

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide

<400> 265

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18

<210> 266

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<212> DNA
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<220>
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<400> 266
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<210> 267
<211> 390
<212> DNA
<213> Homo sapiens

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accatgctgt ggataacgct gcccatgagt ccttttgcag aagcagagaa attggcatgg 120
gatctggagg ttggagggtt agctggacag ccccttaaag ttttcaactcc acgtaaaaaa 180
ggttctgggg aagtgggtga tgcttctcag tcgcccagca gaagcaatga tggccagcat 240
tctgcattg gccacagcag agatctctgc tgctacactg ctcagaccct cataatctcc 300
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tgctacgaca gtgttgatta taaaatatag 390

<210> 268
<211> 129
<212> PRT
<213> Homo sapiens

<400> 268
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Leu Ala Ala Val Thr Met Leu Trp Ile Thr Leu Pro Met Ser Pro Phe
20 25 30
Ala Glu Ala Glu Lys Leu Ala Trp Asp Leu Glu Val Gly Gly Leu Ala
35 40 45
Gly Gln Pro Leu Lys Val Phe Thr Pro Arg Lys Lys Gly Ser Gly Glu
50 55 60
Val Gly Asp Ala Ser Gln Ser Pro Ser Arg Ser Asn Asp Gly Gln His
65 70 75 80
Ser Cys Ile Gly His Ser Arg Asp Leu Cys Cys Tyr Thr Ala Gln Thr
85 90 95

Leu Ile Ile Ser Tyr Thr Ser Asn Gly Leu Ser Pro Leu Ala Thr Pro
100 105 110

Pro Phe His Pro Ile Pro Gly Asn Cys Tyr Asp Ser Val Asp Tyr Lys
115 120 125

Ile

<210> 269
<211> 2856
<212> DNA
<213> Homo sapiens

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gaccgctttg ttgccattag caatccactg cactgtaaca tgaccatgac tccaggtagc 420
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gcagcctccg gagcagccac tatgctgaca aaggggctgc ccgacatcac tgtgggactg	1380
cagatttatg actcctgcat ctcagggatc caggctctgg ggagcaccct ggccctgctg	1440
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tctgagagag agggaccatt cctgggaggc acgtatgcca atgcatggga agccaggctt	2040
tctcaggtta acttcaccac caaagcccaa gaagaggttt tcttcgcaa agatggggaa	2100
gtgctgacaa cgtttgacat taaaaacatc tatgttctcc cagacctgtc aggacagaca	2160
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agcgcaattg tctgggcaga aggaccctta aagattagag ctgagagAAC cctaagaacc	2280
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gatagtgttg catgtcagaa gtgctctgac aaccagtggc ccaatgtgca gaagggcgag	2520
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gtctgcacag ccctgctctt tctccttgcc ctggccatct taggcatctt ccatgttgct	2640
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atggccatgg aggtctttgt catcttgga tcagcaggag gcctcatgtc ctccctcttc	2760
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ggccggcatc atcgcaagtg ggaaaaactg aagtga	2856

<210> 270

<211> 951

<212> PRT

<213> Homo sapiens

<400> 270

Met Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val
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Phe Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu
20 25 30

Ser Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu
35 40 45

Ile Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser
50 55 60

His Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln
65 70 75 80

Ile Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys
85 90 95

Arg Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys
100 105 110

Tyr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn
115 120 125

Pro Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe
130 135 140

Leu Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr
145 150 155 160

Thr Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe
165 170 175

Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met
180 185 190

Thr Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu
195 200 205

Ala Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala
210 215 220

Ile Leu Arg Val Lys Ser Ala Gly Gly Leu Leu Ile Ala Ser Ala His
 225 230 235 240
 Phe Asp Ala Tyr Val Tyr Glu Thr Gly Ile Asn Tyr Asn Thr Val Tyr
 245 250 255
 Gly Ser Gly Lys Ala Val Gly Trp Ser Trp Arg Ser Leu Arg Glu Thr
 260 265 270
 Asn His Met Arg Pro Gly Asn Thr Ser Lys His Ser Ala Ala Gln Leu
 275 280 285
 His Gln Cys Leu Ile Gln Gln Val Gly Arg Trp Pro Leu Gln Ser Met
 290 295 300
 Pro Phe Pro Val Ser Ala Gly Pro Pro Tyr Lys Ser Val Gln Pro Leu
 305 310 315 320
 Pro Gly Asp Pro Arg Pro Leu Leu Cys Ile Thr Gly Leu Phe Leu Thr
 325 330 335
 Leu Lys Met Met Gly Cys Gly Pro Arg Arg Pro Arg Asp Arg Lys Ser
 340 345 350
 Asp Phe Phe Ile Asn Thr Asp Pro Gly Ala Gly Ser Pro Glu Glu Gln
 355 360 365
 Arg Cys Gly Trp Glu Gly His Pro Ser His Ser Tyr Thr Leu Gly Leu
 370 375 380
 Ser Leu Pro Val Asn Phe Gly Leu Lys Cys Pro Trp Trp Thr Leu Ser
 385 390 395 400
 Gly Pro Pro Ala Thr Cys Gln Arg Pro Asp Leu Gln Thr Pro Ser Pro
 405 410 415
 Pro Lys Glu Ile Cys Ser Ser Gly Leu Arg Pro Leu Thr His Ser Ala
 420 425 430
 Gly Pro Asp Arg Ser Gln Val Pro Ala Ala Ser Gly Ala Ala Thr Met
 435 440 445
 Leu Thr Lys Gly Leu Pro Asp Ile Thr Val Gly Leu Gln Ile Tyr Asp
 450 455 460

Ser Cys Ile Ser Gly Ile Gln Ala Leu Gly Ser Thr Leu Ala Leu Leu
 465 470 475 480

Ser Asn Gln Leu Pro Pro Thr Thr Asn Tyr Ala Cys Gly Ser Gln Gln
 485 490 495

His Leu Leu Gly Val Val Gly Gly Met Thr Phe Leu Glu Ser Glu Pro
 500 505 510

Met Ser Glu Leu Leu Ser Ile Tyr Arg Val Pro Gln Gly Gln Arg Leu
 515 520 525

Thr Lys Asn Phe Glu Val Lys Glu Leu Val Cys Thr Tyr Leu Val Gly
 530 535 540

Gln Leu Pro Tyr Gly Leu Val Ser Tyr Asp Asn Ser Asn Phe Glu Trp
 545 550 555 560

Leu Asp Gln Gln Leu Gln Lys Gln Ile Gly Gly Glu Gly Leu Pro Val
 565 570 575

Gly Ala Ala Pro Ser Arg Val Ala Arg Gln Gln Ser Asp Glu Glu Ala
 580 585 590

Val Gly Gly Val Gln Gly Tyr Arg Trp Ser Gly Leu Gly Ala Ser Ile
 595 600 605

Gln Ser Ala Arg Glu Gly Ala Trp His Arg Thr Gly Leu Glu Asn Met
 610 615 620

Thr Thr Ala His Leu Ser Ala Phe Lys Leu Pro Asp Leu Thr Ala Thr
 625 630 635 640

Tyr Gln Ala Tyr Leu Ala Ala Lys Ala Leu Trp Val Ala Tyr Gln Asn
 645 650 655

Leu Met Ser Cys Ser Glu Arg Glu Gly Pro Phe Leu Gly Gly Thr Tyr
 660 665 670

Ala Asn Ala Trp Glu Ala Arg Leu Ser Gln Val Asn Phe Thr Thr Lys
 675 680 685

Ala Gln Glu Glu Val Phe Phe Ala Lys Asp Gly Glu Val Leu Thr Thr
 690 695 700

Phe	Asp	Ile	Lys	Asn	Ile	Tyr	Val	Leu	Pro	Asp	Leu	Ser	Gly	Gln	Thr
705					710					715					720
Ala	Ile	Val	Gly	His	Phe	Asp	Phe	Arg	Ala	Pro	Ser	Gly	Lys	Glu	Leu
				725					730					735	
Leu	Leu	Asp	Asp	Ser	Ala	Ile	Val	Trp	Ala	Glu	Gly	Pro	Leu	Lys	Ile
			740					745					750		
Arg	Ala	Glu	Arg	Thr	Leu	Arg	Thr	Lys	Thr	Thr	Gln	His	Leu	Ser	His
		755					760					765			
Pro	Lys	Leu	Gln	Glu	Ser	Leu	Pro	Leu	Ser	Ala	Thr	Lys	Asn	Val	Leu
	770					775					780				
Trp	Lys	Pro	Gly	Ser	Gln	Pro	Tyr	Leu	Arg	Ser	Gln	Asn	Ala	Ala	Thr
785					790					795					800
Lys	Ala	Phe	Pro	Asp	Pro	Glu	Glu	Lys	Ser	Gln	Cys	His	Gln	Phe	Leu
				805					810					815	
Phe	Leu	Pro	Ser	Asp	Ser	Val	Ala	Cys	Gln	Lys	Cys	Ser	Asp	Asn	Gln
			820					825					830		
Trp	Pro	Asn	Val	Gln	Lys	Gly	Glu	Cys	Ile	Pro	Lys	Thr	Leu	Asp	Phe
		835					840					845			
Leu	Phe	Tyr	His	Lys	Pro	Leu	Asp	Thr	Ala	Leu	Ala	Val	Cys	Thr	Ala
	850					855					860				
Leu	Leu	Phe	Leu	Leu	Ala	Leu	Ala	Ile	Leu	Gly	Ile	Phe	His	Val	Val
865					870					875					880
Cys	Ser	Cys	Val	Trp	Val	Ser	Phe	Ile	Pro	Ala	His	Met	His	Ala	His
				885					890					895	
Ser	Lys	Asp	Thr	Met	Ala	Met	Glu	Val	Phe	Val	Ile	Leu	Ala	Ser	Ala
			900					905					910		
Gly	Gly	Leu	Met	Ser	Ser	Leu	Phe	Phe	Ser	Lys	Cys	Tyr	Ile	Ile	Leu
		915					920					925			
Leu	His	Pro	Glu	Lys	Asn	Thr	Lys	Asp	Gln	Met	Phe	Gly	Arg	His	His
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Arg Lys Trp Glu Lys Leu Lys
945 950

<210> 271
<211> 956
<212> DNA
<213> Homo sapiens

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tggcggcagt tgctgggcct actccccgag cacatggcgg agaagctgtg tgaggcctgg 180
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tgccggtcaa cctgaggggac gaagtgtggt gtccggcacc cctggagagg cccaaa 956

<210> 272
<211> 231
<212> PRT
<213> Homo sapiens

<400> 272

Ala Ala Leu Tyr Gly Ala Ser Gly His Phe Ala Pro Gly Thr Thr Val
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Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly Ser Ala Thr Pro Asp Asn
20 25 30

Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg Gln Leu Leu Gly Leu Leu
35 40 45

Pro Glu His Met Ala Glu Lys Leu Cys Glu Ala Trp Ala Phe Gly Gln
 50 55 60

Ser His Gln Thr Gly Val Val Ala Leu Gly Leu Leu Thr Cys Leu Leu
 65 70 75 80

Ala Met Leu Leu Ala Gly Arg Ile Arg Leu Arg Arg Ile Asp Ala Phe
 85 90 95

Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly Leu His Leu Ala Glu Gln
 100 105 110

His Leu Gln Ala Ala Ser Pro Ser Trp Leu Asp Thr Leu Lys Phe Ser
 115 120 125

Thr Thr Ser Leu Cys Cys Leu Val Gly Phe Thr Ala Ala Val Ala Thr
 130 135 140

Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg Pro Arg Arg Phe Phe Pro
 145 150 155 160

Gly Asp Ser Ala Gly Leu Phe Pro Thr Ser Pro Ser Leu Ala Ile Pro
 165 170 175

His Pro Ser Val Gly Gly Ser Pro Ala Ser Leu Phe Ile Pro Ser Pro
 180 185 190

Pro Ser Phe Leu Pro Leu Ala Asn Gln Ala Ala Leu Pro Val Ser Ser
 195 200 205

Thr Asp Leu Thr Leu Leu Ile Cys Leu Ala Ala Ser Ala Gly Pro Ser
 210 215 220

Leu Trp Glu Pro Tyr Pro Leu
 225 230

<210> 273
 <211> 1806
 <212> DNA
 <213> Homo sapiens

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tacccccctg ccggcctgcc gtccttccac gcggagagcc atggagggag tgagcgcgct	180
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cgcccagtac ttggagcacc tgaaccacgt ggtgagcagc gcgccagcc tgcgcgaccc	480
ttcgcagccg cagcagtggg tgagcagcca agtcctgctg tgcaagaggt gcaaccacca	540
ccagaccacc aagatcaagc agctggccgc cttcgctccc cgcgaggagg gcaggtatga	600
cgaggaggtc gaggtgtacc ggcacacact ggagcagatg tacaagctgt gccggccgtg	660
ccaagcggct gtggagtact acatcaagca ccagaaccgc cagctgcgcg ccctgttget	720
cagccaccag ttcaagcgcc gggaggccga ccagaccac gcacagaact tctcctccgc	780
cgtgaagtcc ccggtccagg tcatcctgct ccgtgccctc gccttcctgg cctgcgcctt	840
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cagggccttc cgggggcggc tcggtgggccc tccagtccgg ctctctggcc acgggaggcc	1740
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cccaaa	1806

<211> 461
 <212> PRT
 <213> Homo sapiens

<400> 274

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Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu
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Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys
 35 40 45

Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
 50 55 60

Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
 65 70 75 80

Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His
 85 90 95

Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln
 100 105 110

Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln
 115 120 125

Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly
 130 135 140

Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met
 145 150 155 160

Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys
 165 170 175

His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys
 180 185 190

Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val
 195 200 205

Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala
 210 215 220

Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe
 225 230 235 240

Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly
 245 250 255

Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg
 260 265 270

Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu
 275 280 285

Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly
 290 295 300

Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu
 305 310 315 320

Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly
 325 330 335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu
 340 345 350

Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe
 355 360 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg
 370 375 380

Pro Arg Arg Phe Phe Pro Gly Asp Ser Ala Gly Leu Phe Pro Thr Ser
 385 390 395 400

Pro Ser Leu Ala Ile Pro His Pro Ser Val Gly Gly Ser Pro Ala Ser
 405 410 415

Leu Phe Ile Pro Ser Pro Pro Ser Phe Leu Pro Leu Ala Asn Gln Ala
 420 425 430

Ala Leu Pro Val Ser Ser Thr Asp Leu Thr Leu Leu Ile Cys Leu Ala
 435 440 445

Ala Ser Ala Gly Pro Ser Leu Trp Glu Pro Tyr Pro Leu
 450 455 460

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<210> 275
<211> 600
<212> DNA
<213> Homo sapiens

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<222> (460)..(460)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (530)..(530)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (574)..(574)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (577)..(577)
<223> n is a, c, g, t or u

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ctgggcatct tcatcagaga cgtgcacaac ttctgcatca cctaccacta tgaccacatg      180
agctttcact acacggtcgt cctgatgttc tcccagggtga tcagcatctg ctgggctgcc      240
atggggtcac tctatgctga gatgacagaa aacaagtacg tctgcttctc cgccctgacc      300
atcctgagtg agtggcagga gggggagggg gcaagaggga gcggggagct ttggaaccct      360
gagatgtggc aaggagtagc caggaagggt tactggggct catggggggc tctgtcccc      420
gccagtgct caacggagcc atgctcttca accgcctgtn cttggagttt ctggccatcg      480
agtaccggga ggagcaccac tgaggcctgg ggagtcggaa cagggctaan gagggggaag      540
caaaaggctg cctcgggtgt ttaataaag ctgntgntta tttccaaaaa aaaaaaaaaa      600

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<210> 276
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (128)..(128)
<223> Xaa is S, P, T or A

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<220>
 <221> UNSURE
 <222> (151)..(151)
 <223> Xaa is M, T, K or R

<220>
 <221> UNSURE
 <222> (166)..(166)
 <223> Xaa is L, M or V

<220>
 <221> UNSURE
 <222> (167)..(167)
 <223> Xaa is F, L, I or V

<400> 276

Met Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly
 1 5 10 15

Ile Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp
 20 25 30

His Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile
 35 40 45

Ser Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu
 50 55 60

Asn Lys Tyr Val Cys Phe Ser Ala Leu Thr Ile Leu Ser Glu Trp Gln
 65 70 75 80

Glu Gly Glu Gly Ala Arg Gly Ser Gly Glu Leu Trp Asn Pro Glu Met
 85 90 95

Trp Gln Gly Val Ala Arg Glu Gly Tyr Trp Gly Ser Trp Gly Ala Leu
 100 105 110

Ser Pro Ala Gln Cys Ser Thr Glu Pro Cys Ser Ser Thr Ala Cys Xaa
 115 120 125

Trp Ser Phe Trp Pro Ser Ser Thr Gly Arg Ser Thr Thr Glu Ala Trp
 130 135 140

Gly Val Gly Thr Gly Leu Xaa Arg Gly Lys Gln Lys Ala Ala Ser Gly
 145 150 155 160

Val Leu Ile Lys Leu Xaa Xaa Ile Ser Lys Lys Lys Lys Lys
 165 170

<210> 277
 <211> 457
 <212> DNA
 <213> Homo sapiens

<400> 277
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 tcctggtaaa ttcattccca ggaacatcgc tgccactgct attattctag cagctgttcc 120
 catactccaa tgagtccagt taaacatttg ccttcctggg tcatgtaaag gtggcctgaa 180
 gactgccaga agaggctgaa gaactgccaa agtcatcact atacagccga ggtatgggtg 240
 gtaacctgca tgccactcc agcctcccct gtatataaac ggcataacaa aagcaatgca 300
 ggtgaggaca gttgtggtga acatgagcat cccatgcacc tgaaaccaag ctgcttcacc 360
 aagcaagaaa gcttttgacc aaactggctt gaagaaccgg gcaaccagta cacctatgct 420
 aacagtagtc atccatgccaa caaacattaa ggcacca 457

<210> 278
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 278
 Met Phe Val Ala Trp Met Thr Thr Val Ser Ile Gly Val Leu Val Ala
 1 5 10 15
 Arg Phe Phe Lys Pro Val Trp Ser Lys Ala Phe Leu Leu Gly Glu Ala
 20 25 30
 Ala Trp Phe Gln Val His Arg Met Leu Met Phe Thr Thr Thr Val Leu
 35 40 45
 Thr Cys Ile Ala Phe Val Met Pro Phe Ile Tyr Arg Gly Gly Trp Ser
 50 55 60
 Arg His Ala Gly Tyr His Pro Tyr Leu Gly Cys Ile Val Met Thr Leu
 65 70 75 80
 Ala Val Leu Gln Pro Leu Leu Ala Val Phe Arg Pro Pro Leu His Asp
 85 90 95
 Pro Arg Arg Gln Met Phe Asn Trp Thr His Trp Ser Met Gly Thr Ala
 100 105 110
 Ala Arg Ile Ile Ala Val Ala Ala Met Phe Leu Gly Met Asn Leu Pro

115

120

125

Gly Leu Asn Leu Pro Asp Ser Trp Lys Thr Tyr Ala Met Thr Asp Ser
 130 135 140

<210> 279
 <211> 293
 <212> DNA
 <213> Homo sapiens

<400> 279
 tttttttttt tttttttaag gctgaagcaa ataggaacgt atattttctca tgaatccaaa 60
 gcaaagacac aggaagtgtt ggcattcttt tgggtggctgg tagctcttga ctttctcttc 120
 aagggttgcca catgccttag cagcagctca tgacttcacg ttctcaccgt attcgaaggc 180
 aggaagcatg gagtagctgg cagctgcgtt tgacacagac tgccctcgga ccccttctcc 240
 gcgcagtgcg actcgcaatt gtctggagca cgttggcagc agccctcgtg ccg 293

<210> 280
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 280
 Arg His Glu Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His
 1 5 10 15

Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Leu Pro
 20 25 30

Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val Arg Thr
 35 40 45

<210> 281
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 281
 Cys Gln Lys Gln Arg Asn Trp His Gly Ile Trp Arg Leu Glu Val
 1 5 10 15

<210> 282
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 282

Met Ala Lys Gln Gly Glu Met Asn Thr Ser Thr Ser Cys
1 5 10

<210> 283
<211> 13
<212> PRT
<213> Homo sapiens

<400> 283

Pro Lys Arg Gly Gly Arg Ala Gly Arg Glu His Ser Cys
1 5 10

<210> 284
<211> 91
<212> PRT
<213> Homo sapiens

<400> 284

Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu
1 5 10 15

Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp
20 25 30

Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe
35 40 45

Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met
50 55 60

Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly
65 70 75 80

Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr
85 90

<210> 285
<211> 15
<212> PRT
<213> Homo sapiens

<400> 285

Cys Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser
1 5 10 15

<210> 286
<211> 14

<212> PRT
<213> Homo sapiens

<400> 286

Cys Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr
1 5 10

<210> 287
<211> 19
<212> PRT
<213> Homo sapiens

<400> 287

Met Ala Cys Ile Tyr Pro Thr Thr Phe Tyr Thr Ser Leu Pro Thr Lys
1 5 10 15

Ser Leu Asn

<210> 288
<211> 121
<212> PRT
<213> Homo sapiens

<400> 288

Ala Pro Pro Ser Cys Arg Glu Cys Tyr Gln Ser Leu His Tyr Arg Gly
1 5 10 15

Glu Met Gln Gln Tyr Phe Thr Tyr His Thr His Ile Glu Arg Ser Cys
20 25 30

Tyr Gly Asn Leu Ile Glu Glu Cys Val Glu Ser Gly Lys Ser Tyr Tyr
35 40 45

Lys Val Lys Asn Leu Gly Val Cys Gly Ser Arg Asn Gly Ala Ile Cys
50 55 60

Pro Arg Gly Lys Gln Trp Leu Cys Phe Thr Lys Ile Gly Gln Trp Gly
65 70 75 80

Val Asn Thr Gln Val Leu Glu Asp Ile Lys Arg Glu Gln Ile Ile Ala
85 90 95

Lys Ala Lys Ala Ser Lys Pro Thr Thr Pro Pro Glu Asn Arg Pro Arg
100 105 110

His Phe His Ser Phe Ile Gln Lys Leu

115

120

<210> 289
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 289

Cys Glu Asn Arg Pro Arg His Phe His Ser Phe Ile Gln Lys Leu
 1 5 10 15

<210> 290
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 290

Cys Ile Tyr Pro Thr Thr Phe Tyr Thr Ser Leu Pro Thr
 1 5 10

<210> 291
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 291

Cys Lys Glu Asp Glu Leu Val Arg Asp Ser Pro Ala Arg Lys
 1 5 10

<210> 292
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 292

Ala Leu Gly Thr Arg Leu Ser Gln His Thr Asp Val
 1 5 10

<210> 293
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 293

Asp Phe Asn Cys Pro Cys Leu Val His Tyr Asn
 1 5 10

<210> 294
 <211> 53

<212> PRT
 <213> Homo sapiens

 <400> 294

 Ser Ser Ser Val Asp Pro Glu Lys Phe Leu Asp Phe Ala Asn Met Thr
 1 5 10 15

 Pro Ser Gln Val Gln Leu Phe Leu Ala Lys Val Pro Cys Lys Glu Asp
 20 25 30

 Glu Leu Val Arg Asp Ser Pro Ala Arg Lys Ala Val Ser Arg Tyr Leu
 35 40 45

 Arg Cys Leu Ser Gln
 50

 <210> 295
 <211> 146
 <212> PRT
 <213> Homo sapiens

 <400> 295

 Arg Cys Leu Arg Pro Cys Phe Asp Gln Thr Val Phe Leu Gln Arg Arg
 1 5 10 15

 Tyr Trp Ser Asn Tyr Val Asp Leu Glu Gln Lys Leu Phe Asp Glu Thr
 20 25 30

 Cys Cys Glu His Ala Arg Asp Phe Ala His Arg Cys Val Leu His Phe
 35 40 45

 Phe Ala Ser Met Arg Ser Glu Leu Gln Ala Arg Gly Leu Arg Arg Gly
 50 55 60

 Asn Ala Gly Arg Arg Leu Glu Leu Pro Ala Val Pro Glu Pro Pro Glu
 65 70 75 80

 Gly Leu Asp Ser Gly Ser Gly Lys Ala His Leu Arg Ala Ile Ser Ser
 85 90 95

 Arg Glu Gln Val Asp Arg Leu Leu Ser Thr Trp Tyr Ser Ser Lys Pro
 100 105 110

 Pro Leu Asp Leu Ala Ala Ser Pro Gly Leu Cys Gly Gly Gly Leu Ser
 115 120 125

His Arg Ala Pro Thr Leu Ala Leu Gly Thr Arg Leu Ser Gln His Thr
 130 135 140

Asp Val
 145

<210> 296
 <211> 1035
 <212> PRT
 <213> Homo sapiens

<400> 296

Met Pro Cys Gly Phe Ser Pro Ser Pro Val Ala His His Leu Val Pro
 1 5 10 15

Gly Pro Pro Asp Thr Pro Ala Gln Gln Leu Arg Cys Gly Trp Thr Val
 20 25 30

Gly Gly Trp Leu Leu Ser Leu Val Arg Gly Leu Leu Pro Cys Leu Pro
 35 40 45

Pro Gly Ala Arg Thr Ala Glu Gly Pro Ile Met Val Leu Ala Gly Pro
 50 55 60

Leu Ala Val Ser Leu Leu Leu Pro Ser Leu Thr Leu Leu Val Ser His
 65 70 75 80

Leu Ser Ser Ser Gln Asp Val Ser Ser Glu Pro Ser Ser Glu Gln Gln
 85 90 95

Leu Cys Ala Leu Ser Lys His Pro Thr Val Ala Phe Glu Asp Leu Gln
 100 105 110

Pro Trp Val Ser Asn Phe Thr Tyr Pro Gly Ala Arg Asp Phe Ser Gln
 115 120 125

Leu Ala Leu Asp Pro Ser Gly Asn Gln Leu Ile Val Gly Ala Arg Asn
 130 135 140

Tyr Leu Phe Arg Leu Ser Leu Ala Asn Val Ser Leu Leu Gln Ala Thr
 145 150 155 160

Glu Trp Ala Ser Ser Glu Asp Thr Arg Arg Ser Cys Gln Ser Lys Gly
 165 170 175

Lys Thr Glu Glu Glu Cys Gln Asn Tyr Val Arg Val Leu Ile Val Ala

180

185

190

Gly Arg Lys Val Phe Met Cys Gly Thr Asn Ala Phe Ser Pro Met Cys
195 200 205

Thr Ser Arg Gln Val Gly Asn Leu Ser Arg Thr Ile Glu Lys Ile Asn
210 215 220

Gly Val Ala Arg Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val
225 230 235 240

Ile Ser Ser Gln Gly Glu Leu Tyr Ala Ala Thr Val Ile Asp Phe Ser
245 250 255

Gly Arg Asp Pro Ala Ile Tyr Arg Ser Leu Gly Ser Gly Pro Pro Leu
260 265 270

Arg Thr Ala Gln Tyr Asn Ser Lys Trp Leu Asn Glu Pro Asn Phe Val
275 280 285

Ala Ala Tyr Asp Ile Gly Leu Phe Ala Tyr Phe Phe Leu Arg Glu Asn
290 295 300

Ala Val Glu His Asp Cys Gly Arg Thr Val Tyr Ser Arg Val Ala Arg
305 310 315 320

Val Cys Lys Asn Asp Val Gly Gly Arg Phe Leu Leu Glu Asp Thr Trp
325 330 335

Thr Thr Phe Met Lys Ala Arg Leu Asn Cys Ser Arg Pro Gly Glu Val
340 345 350

Pro Phe Tyr Tyr Asn Glu Leu Gln Ser Ala Phe His Leu Pro Glu Gln
355 360 365

Asp Leu Ile Tyr Gly Val Phe Thr Thr Asn Val Asn Ser Ile Ala Ala
370 375 380

Ser Ala Val Cys Ala Phe Asn Leu Ser Ala Ile Ser Gln Ala Phe Asn
385 390 395 400

Gly Pro Phe Arg Tyr Gln Glu Asn Pro Arg Ala Ala Trp Leu Pro Ile
405 410 415

Ala Asn Pro Ile Pro Asn Phe Gln Cys Gly Thr Leu Pro Glu Thr Gly

420

425

430

Pro Asn Glu Asn Leu Thr Glu Arg Ser Leu Gln Asp Ala Gln Arg Leu
 435 440 445

Phe Leu Met Ser Glu Ala Val Gln Pro Val Thr Pro Glu Pro Cys Val
 450 455 460

Thr Gln Asp Ser Val Arg Phe Ser His Leu Val Val Asp Leu Val Gln
 465 470 475 480

Ala Lys Asp Thr Leu Tyr His Val Leu Tyr Ile Gly Thr Glu Ser Gly
 485 490 495

Thr Ile Leu Lys Ala Leu Ser Thr Ala Ser Arg Ser Leu His Gly Cys
 500 505 510

Tyr Leu Glu Glu Leu His Val Leu Pro Pro Gly Arg Arg Glu Pro Leu
 515 520 525

Arg Ser Leu Arg Ile Leu His Ser Ala Arg Ala Leu Phe Val Gly Leu
 530 535 540

Arg Asp Gly Val Leu Arg Val Pro Leu Glu Arg Cys Ala Ala Tyr Arg
 545 550 555 560

Ser Gln Gly Ala Cys Leu Gly Ala Arg Asp Pro Tyr Cys Gly Trp Asp
 565 570 575

Gly Lys Gln Gln Arg Cys Ser Thr Leu Glu Asp Ser Ser Asn Met Ser
 580 585 590

Leu Trp Thr Gln Asn Ile Thr Ala Cys Pro Val Arg Asn Val Thr Arg
 595 600 605

Asp Gly Gly Phe Gly Pro Trp Ser Pro Trp Gln Pro Cys Glu His Leu
 610 615 620

Asp Gly Asp Asn Ser Gly Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp
 625 630 635 640

Ser Pro Arg Pro Arg Cys Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile
 645 650 655

His Ile Ala Asn Cys Ser Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser

660	665	670
Trp Ala Leu Cys Ser Thr Ser Cys Gly Ile Gly Phe Gln Val Arg Gln		
675	680	685
Arg Ser Cys Ser Asn Pro Ala Pro Arg His Gly Gly Arg Ile Cys Val		
690	695	700
Gly Lys Ser Arg Glu Glu Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro		
705	710	715 720
Val Pro Ile Phe Trp Ala Ser Trp Gly Ser Trp Ser Lys Cys Ser Ser		
	725	730 735
Asn Cys Gly Gly Gly Met Gln Ser Arg Arg Arg Ala Cys Glu Asn Gly		
	740	745 750
Asn Ser Cys Leu Gly Cys Gly Val Glu Phe Lys Thr Cys Asn Pro Glu		
	755	760 765
Gly Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr Pro Trp Leu Pro		
	770	775 780
Val Asn Val Thr Gln Gly Gly Ala Arg Gln Glu Gln Arg Phe Arg Phe		
785	790	795 800
Thr Cys Arg Ala Pro Leu Ala Asp Pro His Gly Leu Gln Phe Gly Arg		
	805	810 815
Arg Arg Thr Glu Thr Arg Thr Cys Pro Ala Asp Gly Ser Gly Ser Cys		
	820	825 830
Asp Thr Asp Ala Leu Val Glu Val Leu Leu Arg Ser Gly Ser Thr Ser		
	835	840 845
Pro His Thr Val Ser Gly Gly Trp Ala Ala Trp Gly Pro Trp Ser Ser		
	850	855 860
Cys Ser Arg Asp Cys Glu Leu Gly Phe Arg Val Arg Lys Arg Thr Cys		
865	870	875 880
Thr Asn Pro Glu Pro Arg Asn Gly Gly Leu Pro Cys Val Gly Asp Ala		
	885	890 895
Ala Glu Tyr Gln Asp Cys Asn Pro Gln Ala Cys Pro Val Arg Gly Ala		

900	905	910
Trp Ser Cys Trp Thr Ser Trp Ser Pro Cys Ser Ala Ser Cys Gly Gly		
915	920	925
Gly His Tyr Gln Arg Thr Arg Ser Cys Thr Ser Pro Ala Pro Ser Pro		
930	935	940
Gly Glu Asp Ile Cys Leu Gly Leu His Thr Glu Glu Ala Leu Cys Ala		
945	950	955 960
Thr Gln Ala Cys Pro Glu Gly Trp Ser Pro Trp Ser Glu Trp Ser Lys		
	965	970 975
Cys Thr Asp Asp Gly Ala Gln Ser Arg Ser Arg His Cys Glu Glu Leu		
	980	985 990
Leu Pro Gly Ser Ser Ala Cys Ala Gly Asn Ser Ser Gln Ser Arg Pro		
	995	1000 1005
Cys Pro Tyr Ser Glu Ile Pro Val Ile Leu Pro Ala Ser Ser Met		
	1010	1015 1020
Glu Glu Ala Thr Asp Cys Ala Gly Phe Asn Leu Ile		
	1025	1030 1035

<210> 297
 <211> 16
 <212> PRT
 <213> Homo sapiens

<400> 297

Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val Ile Ser Ser Gln
1 5 10 15

<210> 298
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 298

Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr
1 5 10

<210> 299
 <211> 35
 <212> PRT

<213> Homo sapiens

<400> 299

Glu Arg Val Trp Ser Asp Asp His Lys Asp Phe Asp Cys Asn Thr Arg
1 5 10 15

Gln Pro Gly Cys Ser Asn Val Cys Phe Asp Glu Phe Phe Pro Val Ser
20 25 30

His Val Arg
35

<210> 300

<211> 38

<212> PRT

<213> Homo sapiens

<400> 300

His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro Val Val Lys Cys His
1 5 10 15

Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe Ile Ser Lys Pro Ser
20 25 30

Glu Lys Asn Ile Phe Thr
35

<210> 301

<211> 15

<212> PRT

<213> Homo sapiens

<400> 301

Cys Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile Leu
1 5 10 15

<210> 302

<211> 13

<212> PRT

<213> Homo sapiens

<400> 302

Glu Arg Val Trp Ser Asp Asp His Lys Asp Phe Asp Cys
1 5 10

<210> 303

<211> 38

<212> PRT

<213> Homo sapiens

<400> 303

Asn Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly
1 5 10 15

Ser Asn Gln Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser Asp
20 25 30

Asp Ser Ser Ser Arg Ile
35

<210> 304

<211> 15

<212> PRT

<213> Homo sapiens

<400> 304

Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly Ser Asn Gln Asp
1 5 10 15

<210> 305

<211> 12

<212> PRT

<213> Homo sapiens

<400> 305

Cys Val Pro His Ser Arg Ser Arg Gly Pro Asn Leu
1 5 10

<210> 306

<211> 12

<212> PRT

<213> Homo sapiens

<400> 306

Cys Glu Leu Ser Gln Thr Pro His Pro His Ser Arg
1 5 10

<210> 307

<211> 14

<212> PRT

<213> Homo sapiens

<400> 307

Cys Leu Asp Ser Ala Gly Asn Asn Ala Gly Ile Gln Trp Gly
1 5 10

<210> 308
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 308

Cys Asn Arg Val Ser Lys Asn Pro Glu Met Leu Gln Thr Gly
 1 5 10

<210> 309
 <211> 2115
 <212> DNA
 <213> Homo sapiens

<400> 309

atgcgtatat gttatgaatg ccaaaatgaa agaacattgt ggcgatgtgt ttcccaggat	60
ggggctgact acagtgtggg cgtgtgtgtc cctgattctt gtgctgaaga ggatgtgact	120
ctgatgtctc ggctggatac tttaagattc agaaatactt catttttggc cccttcctc	180
tttcttttta caataaattc ttctctcttg tctgggtgga gtgtgaccag atgtgtgtgt	240
ggaaagatcc ccctggacac atttgctgcc gtatgtctgt tcatcacctt gctgggtctc	300
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acatcgcggg aacacgggga acctctggcc acttacggga gtctgccact gagcgaggcg	420
gagagcaatg aacaaagaag cagaatccca cggacacact gccgggcaca tctcctctg	480
tcagcagcct ccagcagagg aaaaaggttt ctaggagccg tggctcatgc tctggagtgc	540
ttttcttggc agaagaatgt gccagccatc tggactacaa aggcaccagg tggcacctgc	600
tctgcactga atggcattcg tgtcttgagt cttctttgga tcatctcggg acacaccagt	660
cagatgactg catggctgtc tttgggatgg aaagatggag ggcacgaaag gccactggtc	720
atgtctgggc catcagtggg aatcggagac accagagaag ccacgagtgg ttggttaagt	780
gcaagttcgt ttttaaagat gcatcagaat tcagacaaag gaataacccc caaaggcata	840
ctcagatact ttctcagtca cctggtaagg ttgcagcctc ttcacctgta ttcaatgtgc	900
ttgttggttg gactgttctc tcttgttccc tggggacctg tctgggaaat gcccaaattc	960
cactgggata actgccggca agcatggtgg acgaatctgc tgttgctaaa taactttgtg	1020
tcgggtcaaga atgcgtgcaa tggctggacc tggtagcttg ccaatgactt ccagttccac	1080
ctcaccacac cagtgattat cttcatccat gtaaagagta cacagatcct cactcctctt	1140
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cttctgtcgt tggctccatc agaaaccagg acttcccggg gagggctgtt gaatgccagg	1260
ctgttcaccc tgtgcccttt ggttcattga aaaagtgggt atgaaacttt tgggtctggat	1320

gggaaagctg attgccttct tgcttccaaa cttctgaacc tttcaacctg cactggaaat 1380
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 gaaaacattc tcagaaccaa gctgcagctc tctaccaagc cctccaccgg accctgtggg 1680
 cggcggtgt gggctgagtc ctctttgcgt gccacggagg atatggaggt atggaagcgg 1740
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 aggagagcca agcagataaa aggccttcaat ggaaaagaat cttctccagg tctggtgaac 1860
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 gtgcatccga ttctgatcat cctttacaat ggccttcagg aaacacttat tcaccacact 1980
 gacaccaaca tgttctatct tttctctgga caccgtgtgc tgaccttcgt cactgggctg 2040
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 gaatgttctg gttaa 2115

<210> 310
 <211> 704
 <212> PRT
 <213> Homo sapiens

<400> 310

Met Arg Ile Cys Tyr Glu Cys Gln Asn Glu Arg Thr Leu Trp Arg Cys
 1 5 10 15

Val Ser Gln Asp Gly Ala Asp Tyr Ser Val Gly Val Cys Val Pro Asp
 20 25 30

Ser Cys Ala Glu Glu Asp Val Thr Leu Met Ser Arg Leu Asp Thr Leu
 35 40 45

Arg Phe Arg Asn Thr Ser Phe Leu Ala Pro Ser Leu Phe Leu Phe Thr
 50 55 60

Ile Asn Ser Ser Ser Leu Ser Gly Gly Ser Val Thr Arg Cys Ala Ala
 65 70 75 80

Gly Lys Ile Pro Leu Asp Thr Phe Ala Ala Val Cys Leu Phe Ile Thr
 85 90 95

Leu Leu Gly Leu Ile Leu Pro Pro Ala Gly Thr Val Cys Val Ala Ala
 100 105 110

Arg Glu Trp Gly Ser Ala Cys Arg Thr Ser Arg Glu His Gly Glu Pro
 115 120 125

Leu Ala Thr Tyr Gly Ser Leu Pro Leu Ser Glu Ala Glu Ser Asn Glu
 130 135 140

Gln Arg Ser Arg Ile Pro Arg Thr His Cys Arg Ala His Leu Leu Leu
 145 150 155 160

Ser Ala Ala Ser Ser Arg Gly Lys Arg Phe Leu Gly Ala Val Ala His
 165 170 175

Ala Leu Glu Cys Phe Ser Trp Gln Lys Asn Val Pro Ala Ile Trp Thr
 180 185 190

Thr Lys Ala Pro Gly Gly Thr Cys Ser Ala Leu Asn Gly Ile Arg Val
 195 200 205

Leu Ser Leu Leu Trp Ile Ile Ser Gly His Thr Ser Gln Met Thr Ala
 210 215 220

Trp Leu Ser Leu Gly Trp Lys Asp Gly Gly His Glu Arg Pro Leu Val
 225 230 235 240

Met Ser Gly Pro Ser Val Gly Ile Gly Asp Thr Arg Glu Ala Thr Ser
 245 250 255

Gly Trp Leu Ser Ala Ser Ser Phe Leu Lys Met His Gln Asn Ser Asp
 260 265 270

Lys Gly Ile Thr Pro Lys Gly Ile Leu Arg Tyr Phe Leu Ser His Leu
 275 280 285

Val Arg Leu Gln Pro Leu His Leu Tyr Ser Met Cys Leu Leu Val Gly
 290 295 300

Leu Phe Ser Leu Val Pro Trp Gly Pro Val Trp Glu Met Pro Lys Phe
 305 310 315 320

His Trp Asp Asn Cys Arg Gln Ala Trp Trp Thr Asn Leu Leu Leu Leu
 325 330 335

Asn Asn Phe Val Ser Val Lys Asn Ala Cys Asn Gly Trp Thr Trp Tyr
 340 345 350

Leu Ala Asn Asp Phe Gln Phe His Leu Thr Thr Pro Val Ile Ile Phe
 355 360 365

Ile His Val Lys Ser Thr Gln Ile Leu Ile Leu Leu Gly Ala Met Leu
 370 375 380

Phe Leu Ala Ser Phe Thr Ala Thr Ala Leu Ile Thr Leu Ala Tyr Lys
 385 390 395 400

Leu Pro Val Val Ala Pro Ser Glu Thr Arg Thr Ser Arg Gly Gly Leu
 405 410 415

Leu Asn Ala Arg Leu Phe Thr Leu Cys Pro Leu Val His Gly Lys Ser
 420 425 430

Gly Tyr Glu Thr Phe Gly Leu Asp Gly Lys Ala Asp Cys Leu Leu Ala
 435 440 445

Ser Lys Leu Leu Asn Leu Ser Thr Cys Thr Gly Asn Glu Gln Val Cys
 450 455 460

Pro Lys Cys Thr Phe Gly Leu Ala Asp Tyr Ser Asn Gly His Leu Arg
 465 470 475 480

Asp Leu Asp Ser Leu Cys His Val Gln Ile Lys His Asn Ile Leu Ala
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Tyr Phe Leu Val Phe Phe Ser Glu Glu Ala Ile Val Leu Tyr Phe Val
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Glu Tyr Tyr Thr Lys Pro Tyr Cys Arg Phe Gly Pro Val Leu Val Gly
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Leu Phe Leu Ser Ile Tyr Met His Gln Asn His Gln Glu Asn Ile Leu
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Arg Thr Lys Leu Gln Leu Ser Thr Lys Pro Ser Thr Gly Pro Cys Gly
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Arg Arg Leu Trp Ala Glu Ser Ser Leu Arg Ala Thr Glu Asp Met Glu
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Val Trp Lys Arg Leu Gln Ala Leu Leu Ser Gly Ser His Pro Val Pro
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Leu Lys Val Thr Asn Arg Thr His Arg Arg Ala Lys Gln Ile Lys Gly
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Phe Asn Gly Lys Glu Ser Ser Pro Gly Leu Val Asn Arg Val Leu Ser
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Trp Asp Ile Trp Ser Phe Leu Ser Ser Ile Ser Tyr Ala Arg Tyr Leu
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Val His Pro Ile Leu Ile Ile Leu Tyr Asn Gly Leu Gln Glu Thr Leu
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Ile His His Thr Asp Thr Asn Met Phe Tyr Leu Phe Ser Gly His Arg
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Val Leu Thr Phe Val Thr Gly Leu Ala Leu Thr Leu Phe Ile Glu Lys
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Pro Cys Gln Glu Leu Lys Gln His Leu Leu Gly His Glu Cys Ser Gly
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